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Schnable et al.

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(54) QTL REGULATING EAR PRODUCTIVITY TRAITS IN MAIZE

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(51) **Int. Cl.**
A01H 1/04 (2006.01)

(52) **U.S. Cl.**
USPC **800/267**; 800/275

(58) **Field of Classification Search**
None
See application file for complete search history.

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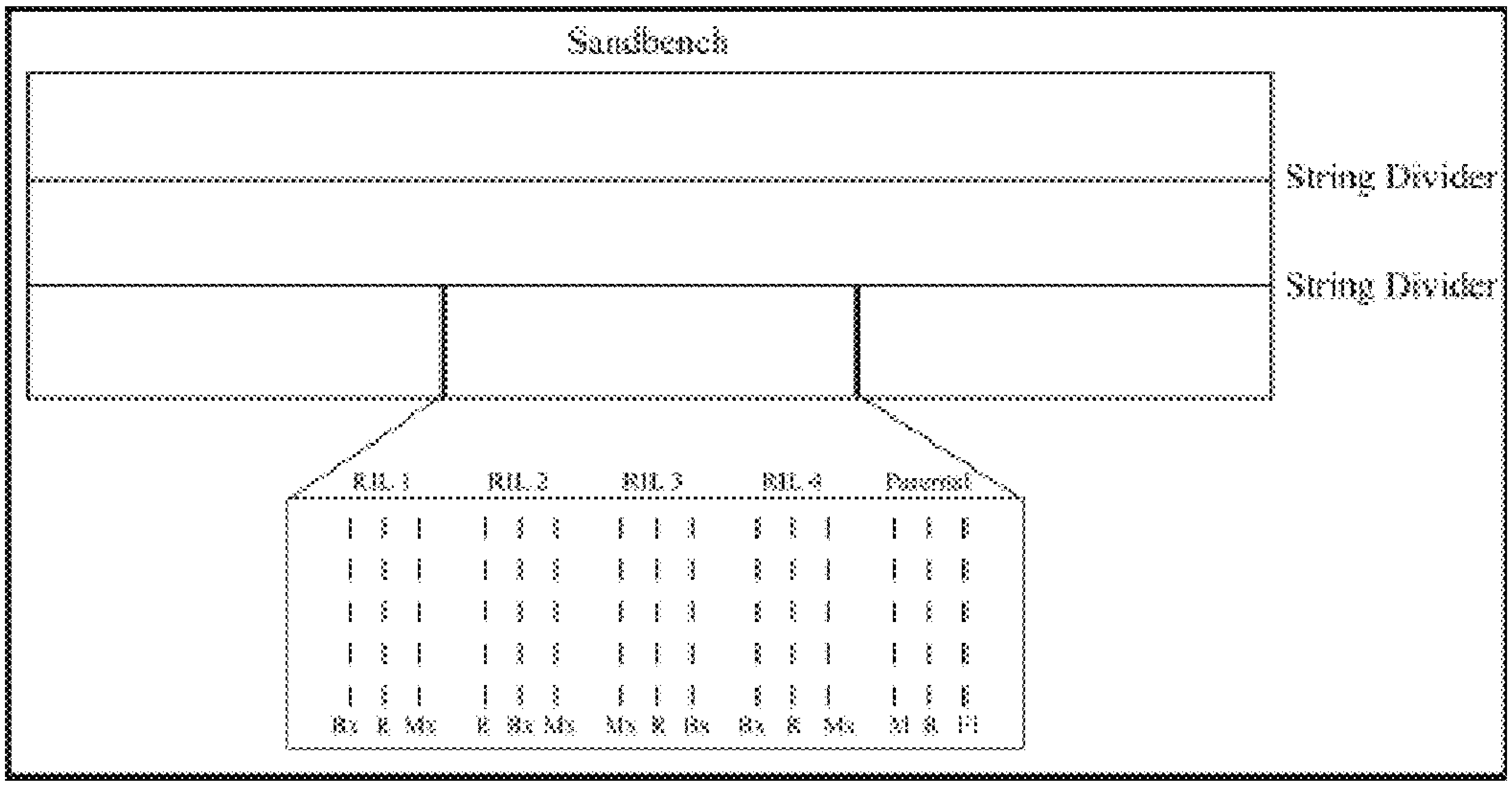
(57) ABSTRACT

The present invention relates to a method for determining an ear productivity trait in maize, which involves analyzing genomic DNA from a maize plant, germplasm, pollen, or seed for the presence of a molecular marker linked to a QTL associated with an ear productivity trait in maize. Also disclosed are methods of selecting a maize plant with a desired ear productivity trait; reliably and predictably introgressing an improved ear productivity trait into a maize line; and producing a maize line having a desired ear productivity trait. A kit for selecting a maize plant by marker assisted selection of a QTL associated with a desired ear productivity trait; an isolated nucleic acid comprising a QTL associated with an ear productivity trait in maize; and a transgenic plant comprising a recombinant nucleic acid genetically linked to a locus in maize, are also disclosed.

16 Claims, 31 Drawing Sheets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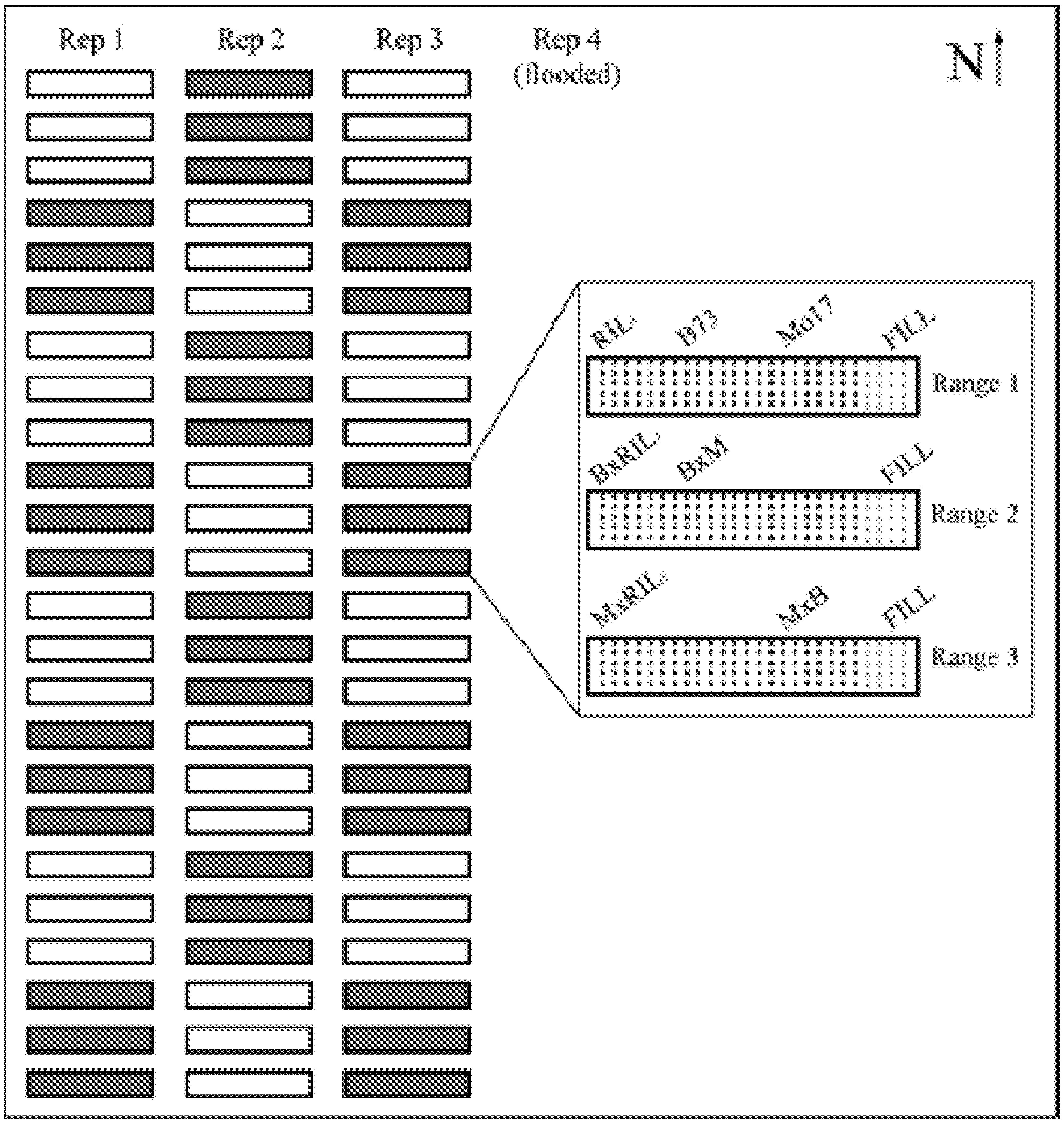
M B F1

Figure 1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Range 1
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BxM
FILL
Range 2
MxRIL
MxB
FILL
Range 3

Figure 2

Marker	SNP Context Seq	SEQ ID NO:
SNP_35511	CGGCTGGCTCAACGAGTGACTTTTTTTTGCGTCTGTATACCTATGTATGTATCTGTCATG[G/C]TACAAGTTCGCTATATGCTGATTTAATAATAAGAGAGAACTTACTAGTAGACTATTGTAT	SEQ ID NO:1
SNP_98111	AGGCTACAAACACAAGAACCACAACATCTGCGTGCGTAGGCAGAGACTCAAAAGGCCAGC[C/T]CTGTATGAAAATTCTAATGATACAATCCTTCAAGGTGATCGACGAAGGTATATTCCGTTT	SEQ ID NO:2
SNP_23951	GGATAGCTGCTGCTTCGCAGGCAGTGCGTCCACATGAAGCCTACATTCAGAGCCATCACA[T/G]GCCTATGCAAGCTTCTGCCCACAACAATCTCCTGTTGTCAATCTGATACTTTTGAGCACG	SEQ ID NO:3
SNP_79262	GGTTTGTGTGTTTTTATGTCAAGACCTCACGCATATCGCGCGGAGTAGCTAAGCTCCACC[G/A]TATATTGGTTGCGACGTATGATCCTTGTTTTATTTAAGTGTGTTGGCGGTTTTATC	SEQ ID NO:4
SNP_19249	TGCCTTGATACATTGTTACAGAGAAACAAAATCAAAAACTTAAGAATGTCCGATACATCT[T/G]CTGTGAATGCACAATACAGTCACACGGCCACTTTTATAAAAGGAAAACGGACCTATCGCC	SEQ ID NO:5
SNP_0984	TTGATGATGGTAATATGTATTCTCAGACTCGACACATGTGTGCAACTCATTTAACACACC[G/A]CCACAGGAAGGTAAGCTTCGCAATCCGATAGAGGGATGCTTACAAATACGCCTAAATCAT	SEQ ID NO:6
SNP_99055	TTTGTGCGTCCTTGTTTCTTTTCTTTTTTCCAGTGAGAGAGAGAGAGAGCTGGCTAAAGA[T/C]GAGGGAGAAGCTGGCACGTAATAGGGTCGATAGTTAAGCATGATCATCCTGTGTATTTGC	SEQ ID NO:7
SNP_77055	TTGTATCGGTTTGTTCAGAGTTTTACGGTGTGGGAACATTAGTAGAAATGTCATTTCACT[G/T]CCTTCTTTTCCCCGCTGGATCGCATTTCACAAAATATTTCCACCATTCTTGCAGAGAAGC	SEQ ID NO:8
SNP_45551	TTTATCTTACAGAAATACATACCTCAATCATCGGTCTCTCCA[T/G]GCAAAAAGATAACGAAACAAACCTAGACTAATGAGCTGAAGACCAGTATAAAATAGGTCG	SEQ ID NO:9
SNP_30953	CCCATCATCAGATATCTAGATCGAAGCGGGGGTCCGAAGGCAATTCATGAATGGAGTGAC[A/G]ACGATAGGAAGCTAGTACAAACTTTTGATCCATCAGCCATGCACGGCATGGAACGGAACA	SEQ ID NO:10
SNP_84678	TGGTGATTCTGTCTGGTTGATATTTGCTACTGATATTGGTCCCATTTGAGATATGCGTTG[C/A]TGCTAGTCTCGTCTTTCTCTGCGCTTGATTTATCGTTATACATCGCTCCATCGCTCGCTG	SEQ ID NO:11
SNP_89298_2	GGGATGTCTTACTGCAGGGTACGGCTGTTGAAAGGATGCCACAGGTTATGTACAGAAGAC[C/A]GCACACCAGGTTGACGCCAGGAACCCATGTGCGCAAAATGTCATGCCTTGCACCGCACCA	SEQ ID NO:12
SNP_32823	ACCAATTAATTTCTGCAAAGTGAGTAATTCGTCTACAGCTTCATGTGAGGAAGAGCTGTT[G/C]AACAGCGCCCTGAAGGACGAATATGGCATAACCAGAGTATTCGCCTACAGCTTCAAGTAA	SEQ ID NO:13
SNP_4623	ATTTATGTTCATTTCTTCTTTTCTTAAAGAAGCATGCACTAAGAACATGAAGGATGCATG[C/T]CATGGAAAGTTTTTGAAAGTCATTGAAACGTATGAGCTCCTCATGCAATGCATTATTCTC	SEQ ID NO:14
SNP_90941	GTTTTCCTGTACTAAGTATATTGTATATTATTCCAGCAGCGATGTGATCTTCAAATTCAT[C/T]GTGATGTATTCGACACCACGCTAAAGGATGGTCTGAGCAAACTTTCTTCAGCTCCTCAAT	SEQ ID NO:15
SNP_81248	GAAGGGATGTGATGTGTATCTCTTAGGCTAGACTGCTTCAGCTAGTTTTCTGTGACTGCT[A/T]CATGAATCCATGGATTACTGATTTACTGGGCTTGTGCTTTGTGTATGATGCTGCCATCTG	SEQ ID NO:16
SNP_82913	GCTGTGAGCATTCGTTTGTAGGAAAAGTGAGAACGGATGTGTATCAATCCGTGTTGGGTG[A/C]CGATGACTCACGGATGAATCAAATATTTGCGTATATTGCGGCCAAAACAGTTCTATCTGA	SEQ ID NO:17
SNP_93907	TATTCATCCTGCTTCATGTGTAGCTTTCATGGAAATTGTGTATGTAACCCAAATCATGGG[C/T]GCATTACAGACCTAACGGAAAAAAGTCAGTGCTGCGCCTTTAGAATGCAGCTTGCTCTCT	SEQ ID NO:18
SNP_90380	AACCTGGTCAGTACTACTTTAGCACAAACTTTTAGCCGCGTGGAACACTCTCCACAGCAC[T/C]ACCACCGCCACATCGCAAACACTAATTTACGATCCGCGAAATCTACCCCAAGGTGGCACA	SEQ ID NO:19
SNP_49724	TGAGTTATTCTCAGGCTGCGCCACAGAACCATCGATGGAAGTACCCAGCAT[C/T]GTTACGCGCTCAAAACGAAGCACCCACACACAAATGCTACCGGTAAACGGCCAATGCGCT	SEQ ID NO:20
SNP_51496	GATTTTTTGTTCCAGAATTGTTATCTGTAACAAGAACATCTACATCTGTGATGACTCACC[A/G]TTAATAAATGTGTCCCGGTGTACCATTTGTTTTTTTTCTTTGAGCACTGGCAGTAGCAGG	SEQ ID NO:21
SNP_11948	CTCTGTGTATCTACCATCTTGGGATGTACTGAATTGAGTTTGGGACGTGTATCTACCTAC[C/G]ATCTTGTATTGTCAGCTCAAGGATGTAGCAAACTAGTAGCAACTTCAAAAAATGAGATGT	SEQ ID NO:22
SNP_18689	CCCCATAGCAAAGACCGCCTTTCCAGCACGTGATATTTCAACAGCCCAACGATTTCTTAC[A/T]CAGTAATTAAGCATATTCCAGTGAAAATCCAAAGCGACATTTGTGTTAACCAAGCGAATG	SEQ ID NO:23
SNP_61221	ATTACATCAACGAGGGCATTAACAAATCAATCGACTTAAATTTCGTTTCCCCAATGATGC[G/A]ACTTCCAAAGTTCAGCTGTCACATTTCATTTAGATGGACTAAGCTACTGCAGATAATCTA	SEQ ID NO:24

Figure 3A

Marker	**SNP Context Seq**	**SEQ ID NO:**
SNP_105143	AAACTGAGTGCTAAATTTTGTTTCTTGTTACTAACCGTTAAGAATCACGAGATGGTTAAT[G/A]ATGGTTGAGCTTGTCCAGAAAACATGGATAAGTGAGGTCTCAAAAAATGTAGCATCTTTT	SEQ ID NO:25
SNP_84372	AAGTTGACTTGGCTAAGGTCTATTGATTAGATGGATTAAGAGAAGTGTTTCGGCTGCCGA[G/A]GTCGTAATATTATGATTCAACATATAAGTACTAATAATCAGTGGGCAAAGCTTCGTTACT	SEQ ID NO:26
SNP_27764	AAACCACATAGTAGTAGTAGAAGTACATGGTAAAGGACGATGGAACATATATATGACACT[C/G]TTGATAGATCTAACAGATGTTCAACTTGTTCTCCATGGTAAAAACATGTTGTTGAGCAGA	SEQ ID NO:27
SNP_95039	AATTTCGAAGTTCTAAACATCTATTGCCGGGATAAAAATTCTCCATATGAATCTCCTCCC[T/G]AATTCGAGCTTCAGAACACCTAGATAAAAGAGGGATTAGACCTATGCCAGACAAAGCTCT	SEQ ID NO:28
SNP_75795	GCTTGTTGAAGAGAACGCTGGTAACATGTTTGCTATATATCTGGGGAGTCCATTTCGTAG[C/T]GAGGAATGATTACACGGCACCATTCTTATCGTCTTATCCAACCACGGGCTCATGTATATT	SEQ ID NO:29
SNP_70805	AATAATCCAAACAGTATACGGCCCAACCGAGTAACCTCATACAAGAACCTAAAGAGAGAG[G/A]AAAAAACCGCGGATCCAACAACCAATTACACCGTCCCTACTAAGGTAATGTTAAAAAGAA	SEQ ID NO:30
SNP_43846	AGTACTAGTATAAGCACATCATAATAATATATAGTATATATAGGAGGAGTCCATACATAA[C/T]TATGGCATATATATGCAGTACGCACACTACAGTCCAGCAGGCCGGCGGTACGACGGTAGG	SEQ ID NO:31
SNP_98032	TTGGCTTCGTTCGTGCTTTTGCTATATGGTGTAGCGTCCTTGCCTGTAAAGAAATCCCAT[A/G]TCACCAGAAGAATTTGAGACGTCAACAGTCATCAAGTACTATAAAATTTAGATGCCTTTT	SEQ ID NO:32
SNP_63437	ACGCTTGTTGTACCATGCAGCCTCTTGTTGATGTATGTTGGCACTCGTTTGTTTCTCCAA[G/T]GCACGTGTTCGGTAACAGTATATAGATGGCTACCTGTGCGTATGTTGGCGCACTTCATGC	SEQ ID NO:33
SNP_94161	CGCGATTCGGTCACCGAACAAACAAACAAACAAACAACAAACCCCTCCGCGGCACTCATC[T/A]TCAGTCCAAAACGACACTTCCACCCCGGCAACAGTCAAGCTCACTTTCCGCGAGCAGGAG	SEQ ID NO:34
SNP_34738	ATTGTTTTTTCATTGCGAACACTCTAGTAGGCCATTTATCTACGGTTTTTTCACTATATT[C/T]ATTAAGATATTATGAGATTTCACATTGCCTTGTAAAGACAAATCTCTAGCCATGTTTGGT	SEQ ID NO:35
SNP_88270	ATTCACGACCCATTTAATCAGGAACCACGCACAATGTGTATATCATAAATAGAAATCCCC[A/G]ATTGCAGATAACAATTGTGGAATAGAAACGTAATACAAAAGGTAGATTTTAGAAAGGACA	SEQ ID NO:36
SNP_2880	CGTTCAAGTGAGATATTCAATTGTTCAGATATTCAAATTCTTTGAAAAACTCAGCACAAA[C/T]ATTCAAATGTTCAGATATTCAAATTCTTCGAAAATGTTCAGACTTTAGACAAAAAGTAAC	SEQ ID NO:37
SNP_36300	CCACCTCCGAAGATACTGTAGATTCCTATGATCATTTGGCTGCATTGTTCCGGCCACCTG[A/T]CGCCGTCTCGCCGGTTGGAGCAGCAGGACCAAATTCCCTTGCGTGGCTCCTGCTCTTTGC	SEQ ID NO:38
SNP_77712	AGAAATGTTCATTGTCATATTGGGCATCCATCCACAGGCACAGTTCAGCGGGATTTTAAG[T/G]CTGAGTTCATCGCTTTTTCAACCCGTCCGAAGCTACCAACATCAGAGCGGTAGGGGAGGC	SEQ ID NO:39

Figure 3B

Marker	**Forward primer Seq**	**SEQ ID NO:**	**Reverse primer seq**	**SEQ ID NO:**
SNP_35511	ACGTTGGATGGTCTACTAGTAAGTTCTCTC	SEQ ID NO:40	ACGTTGGATGGCGTCTGTATACCTATGTATG	SEQ ID NO:79
SNP_98111	ACGTTGGATGCGTAGGCAGAGACTCAAAAG	SEQ ID NO:41	ACGTTGGATGTACCTTCGTCGATCACCTTG	SEQ ID NO:80
SNP_23951	ACGTTGGATGCAACAGGAGATTGTTGTGGG	SEQ ID NO:42	ACGTTGGATGTGAAGCCTACATTCAGAGCC	SEQ ID NO:81
SNP_79262	ACGTTGGATGCAAGGATCATACGTCGCAAC	SEQ ID NO:43	ACGTTGGATGGTCAAGACCTCACGCATATC	SEQ ID NO:82
SNP_19249	ACGTTGGATGGCCTTGATACATTGTTACAG	SEQ ID NO:44	ACGTTGGATGTAAAAGTGGCCGTGTGACTG	SEQ ID NO:83
SNP_0984	ACGTTGGATGACTCGACACATGTGTGCAAC	SEQ ID NO:45	ACGTTGGATGTGTAAGCATCCCTCTATCGG	SEQ ID NO:84
SNP_99055	ACGTTGGATGTATCGACCCTATTACGTGCC	SEQ ID NO:46	ACGTTGGATGGTGCGTCCTTGTTTCTTTTC	SEQ ID NO:85
SNP_77055	ACGTTGGATGTTGTGAAATGCGATCCAGCG	SEQ ID NO:47	ACGTTGGATGTCAGAGTTTTACGGTGTGGG	SEQ ID NO:86
SNP_45551	ACGTTGGATGACATACCTCAATCATCGGTC	SEQ ID NO:48	ACGTTGGATGACTGGTCTTCAGCTCATTAG	SEQ ID NO:87
SNP_30953	ACGTTGGATGCATGGCTGATGGATCAAAAG	SEQ ID NO:49	ACGTTGGATGGATATCTAGATCGAAGCGGG	SEQ ID NO:88
SNP_84678	ACGTTGGATGGCGATGGAGCGATGTATAAC	SEQ ID NO:50	ACGTTGGATGTTGCTACTGATATTGGTCCC	SEQ ID NO:89
SNP_89298_2	ACGTTGGATGTGTTGAAAGGATGCCACAGG	SEQ ID NO:51	ACGTTGGATGTGACATTTTGCGCACATGGG	SEQ ID NO:90
SNP_32823	ACGTTGGATGTCTGCAAAGTGAGTAATTCG	SEQ ID NO:52	ACGTTGGATGGCGAATACTCTGGTTATGCC	SEQ ID NO:91
SNP_4623	ACGTTGGATGTTGCATGAGGAGCTCATACG	SEQ ID NO:53	ACGTTGGATGGCATGCACTAAGAACATGAAG	SEQ ID NO:92
SNP_90941	ACGTTGGATGATTATTCCAGCAGCCATGTG	SEQ ID NO:54	ACGTTGGATGTCAGACCATCCTTTAGCGTG	SEQ ID NO:93
SNP_81248	ACGTTGGATGGTGATGTGTATCTCTTAGGC	SEQ ID NO:55	ACGTTGGATGGCACAAGCCCAGTAAATCAG	SEQ ID NO:94
SNP_82913	ACGTTGGATGGTTTTGGCCCCAATATACGC	SEQ ID NO:56	ACGTTGGATGCGGATGTGTATCAATCCGTG	SEQ ID NO:95
SNP_93907	ACGTTGGATGGCAGCACTGACTTTTTTCCG	SEQ ID NO:57	ACGTTGGATGCTGCTTCATGTGTAGCTTTC	SEQ ID NO:96
SNP_90380	ACGTTGGATGCACAAACTTTTAGCCGCGTG	SEQ ID NO:58	ACGTTGGATGTCGCCGATCGTAAATTAGTG	SEQ ID NO:97
SNP_49724	ACGTTGGATGTGAGTTATTCTCAGGCTGCG	SEQ ID NO:59	ACGTTGGATGTGTGGGTGCTTCGTTTTGAG	SEQ ID NO:98
SNP_51496	ACGTTGGATGAACAAATGGTACACCGGGAC	SEQ ID NO:60	ACGTTGGATGCAAGAACATCTACATCTGTG	SEQ ID NO:99
SNP_11948	ACGTTGGATGTGCTACATCCTTGAGCTGAC	SEQ ID NO:61	ACGTTGGATGACTGAATTGAGTTTGGGACG	SEQ ID NO:100
SNP_18689	ACGTTGGATGATAGCAAAGACCGCCTTTCC	SEQ ID NO:62	ACGTTGGATGTCGCTTTGGATTTTCACTGG	SEQ ID NO:101
SNP_61221	ACGTTGGATGCGACTTAAATTTCGTTTCCCC	SEQ ID NO:63	ACGTTGGATGCTGCAGTAGCTTAGTCCATC	SEQ ID NO:102

Figure 4A

Marker	**Forward primer Seq**	**SEQ ID NO:**	**Reverse primer seq**	**SEQ ID NO:**
SNP_105143	ACGTTGGATGCCGTTAAGAATCACGAGATG	SEQ ID NO:64	ACGTTGGATGGAGACCTCACTTATCCATGT	SEQ ID NO:103
SNP_84372	ACGTTGGATGGATTAAGAGAAGTCTTTGGGC	SEQ ID NO:65	ACGTTGGATGTAACGAAGCTTTGCCCACTG	SEQ ID NO:104
SNP_27764	ACGTTGGATGGGAGAACAAGTTGAACATCTG	SEQ ID NO:66	ACGTTGGATGGAAGTACATGGTAAAGGACG	SEQ ID NO:105
SNP_95039	ACGTTGGATGGCCGGGATAAAAATTCTCCA	SEQ ID NO:67	ACGTTGGATGTGGCATAGGTCTAATCCCTC	SEQ ID NO:106
SNP_75795	ACGTTGGATGCTTGTTGAAGAGAACGCTGG	SEQ ID NO:68	ACGTTGGATGACGATAAGAATGGTGCCGTG	SEQ ID NO:107
SNP_70805	ACGTTGGATGCCAACCGAGTAACCTCATAC	SEQ ID NO:69	ACGTTGGATGAGTAGGCACCGTCTAATTGG	SEQ ID NO:108
SNP_43846	ACGTTGGATGAGTATATATAGGAGGAGTGC	SEQ ID NO:70	ACGTTGGATGGGACTGTAGTGTGCGTACTG	SEQ ID NO:109
SNP_98032	ACGTTGGATGTGCTATATGGTGTAGCGTCC	SEQ ID NO:71	ACGTTGGATGGTACTTGATGACTGTTGACG	SEQ ID NO:110
SNP_63437	ACGTTGGATGTACCATGCAGCCTCTTGTTG	SEQ ID NO:72	ACGTTGGATGCGCACAGGTAGCCATCTATA	SEQ ID NO:111
SNP_94161	ACGTTGGATGAAACAACAAACCCCTCCGC	SEQ ID NO:73	ACGTTGGATGAAGTGAGCTTGACTGTTGCC	SEQ ID NO:112
SNP_34738	ACGTTGGATGACTACGCCATTTATCTACGG	SEQ ID NO:74	ACGTTGGATGCAGATTTGTCTTTACAAGCC	SEQ ID NO:113
SNP_88270	ACGTTGGATGATCAGGAACCACGCACAATG	SEQ ID NO:75	ACGTTGGATGGTATTACGTTTCTATTCCAC	SEQ ID NO:114
SNP_2880	ACGTTGGATGCAAATTCTTTGAAAAACTCAG	SEQ ID NO:76	ACGTTGGATGGTTACTTTTTGTCTAAAGTC	SEQ ID NO:115
SNP_36300	ACGTTGGATGCATTTGGCTGCATTGTTCCG	SEQ ID NO:77	ACGTTGGATGAAGGGAATTTGGTCCTGCTG	SEQ ID NO:116
SNP_77712	ACGTTGGATGCTTCGGACGGGTTGAAAAAG	SEQ ID NO:78	ACGTTGGATGGTCATATTGGGCATCCATCC	SEQ ID NO:117

Figure 4B

Marker Name	Context Seq	SEQ ID NO:
PZA01216.1	GGTATGTTCATTTTGCTATATTTATGGTGAACCGTTGAATGTGACTGGGATAATGATGT[C/T]AGAAA AGGCATTGAAACTTCTCATCGGTGCCCATCCAGTTAATTTCTACGACCGTAAAAAAATAACCCACTGCA ACTGTTTTACAAGAAGTATTCATGTG	SEQ ID NO:118
PZA01497.1	ATACGTATACCGGAGATGAAAGGAGACGGAGGCAGTGAAGAAATATCCTTTTTTTTCTTCTCRTTTTTC ACGAGGATGCSGTGCACTGCTCCCAGAATGCTGTGTCCAATTTACAAACGCACAGGTGGCACATGAACT AGCAGAGTAGCT[C/T]TMTCTTGAAAGGAAACTGTATTTGGGGTCGATGAACCCTCTGGTGTTATTCT TCAGACKGGTAAACGATKTAAC	SEQ ID NO:119
PZB00183.4	GCTCCAGTTCATCAGSCGGTGSGACTGCGGATGCCTACCCARATAGCTCCTACTAGAGACGTCAGCTTC GTCGGC[A/G]GCGAAGGCGTCCGAATGGCCCGACGCCGCAGGAGGCGACCAGACCGGGACCACGGCGC CCTCTCTGCCGGTCCAGCTGCTCGAAGCCTCCGACGCYGACGGAGCAAGCAGAGCWTCTCGCCTGTGGT TCCGASGCTGCTGGAAGRCGTCGTGCTGGCGAGCGCCRTTGTTGGTTCTACGCGCAGCTGGCGGGGCTT CGGCTCKKGGGTGGAGATGGAGATGCGCGTGGAACGGAACCTGCGCCCTGGTGTCCTCCTCCTC--- GCTGTTCGCTACTRCTAGATCGGCGGAGACCTCTGTTCCAGCTCTGTTC	SEQ ID NO:120
PZA02450.1	GACCTACTCATCATTTTCCTGAACATTTTCCAGAACGGTAACTTGTACATTATGTCTACTGCTGCCATT TTTTAATGAGCCCACGTATCTGACAAAAGTGAAATGTCAAATATCAGGTCAAGGCAAGGACAAAGAAAA GGTGGAGAAACTGCATAT[G/T]TTTCAAACCATAAACGTGACAGAGCTAACGAMAGGTTCATTACTGA CCTCRACACCRTTAGGCCCTATTTTGTTGCGGGATATGAACTTC	SEQ ID NO:121
PZA01993.7	TTGCAATCTCATATCTTGAATCTCACACCAAGCATAATAATTCACATTGAAAG[C/T]GTCTGACCTAT CCTCTAGCAGTTGTCGACAAATTTSTCCAGTT- CATGTACAGTAGAAACCGATGCGTTGCAGTYTCAGAACATCTTCACTTC---AGATA	SEQ ID NO:122
PZA03142.5	AGTGCCCGCGCTTGATGTCCGGGCGCAGGTAGTTGGTCCACCGCAGCCGGCAGCTCTTRCCGCACCGGT TCAGCCCTGCATGCATGC------------------------------CCRCR--- RGTCGCTYAAGAAATGACGAGCACG------ AGGCRAACAACTAGGTCACGCATGCAGCACCAGGMRGC- CGGGC[C/T]GGGCTCGACCGAGGAACAGAGCAC--ACGTA---- CGTACCCGCGAGCTTGGGGAGCATGCGCCAATTTCCGGCRCCGTTGGCCTGGACGTAGTCGACGAGCAG CTTGTCCTCCTCCAGCGCCCACTGTCCCTTCTTGATCCCMTTGCTGTSGCAGCACGGASTTCTYCCCAT GGCGRTCGGTCGCTCTC-----CGTC	SEQ ID NO:123
zb21.1	CTACAAAGTGACCAACCATTTCATCGAATTGCTTCAAACCCGAGAGCCGCAAGATAATAGACGAACGAT CAGCTCCAGCCACCTGTAAGTACAATCACAAA[C/T]RGTAAGAGCAATGGATCACTYGTG-------- ----GAGGCTTGTGTTTACAAATAATRGCCAACAACAKGTTACCTCN-NNNATCCTCAAATAATGG-CC	SEQ ID NO:124
PZA00210.1	TCCCTTAGGAAGTATCTACATCAGCAGGAGCCTCACTCAGTTCCCCTCAACMTAGTGCTGAAATTAGCT CTAGATATYGCTCGYGGAATGAGCTACCTACACTCCCAGGGTATACTCCATAGRGACCTGAAATCAGAG AACRTACTTCTGGGAGAAGATATGTCAGTCAAAGTYGCAGATTTCGGGATTTCATGCTTGGAATCACAG TGTGGAAGTGGCAAGGGGTTTACAGGAACCTACAGGTGGATGGCTCC[A/G]GAGATGATCAAAGAGGA ACATCATACTAGGAAAGTGGACGTGTACAGC	SEQ ID NO:125
PZA02427.1	CMATGGTACACGTAACCCGGACCMGTGGTGACGTCGAAGGGGAMGCGGSTCTCCTCCGGCGACGCGGCG TCTGTGAGCGGCTTGAAGCCCACGAGGATCC[G/T]GGTTACCGCGCTGGGCCGCACCTTGAAGACGTT CTTCCAGCCGCGCTCCTGCCGCGGCACGACGTGCCTCCGCSMCCCGGCCAGGTGGCGGTCGACCCCGCA CGCGCGCGCGTCGTTCCGGCGCTTCATGCAGTCCCTGAASTCGTCCA	SEQ ID NO:126

Figure 5A

Marker Name	Context Seq	SEQ ID NO:
PZA02585.2	CTTCCTGATCTTCTTGGCRGTCGTGCAATTCCCCATGCTGTTCTGGCTCGGCAACATATGTGGCTGACCTTTGATCCTATTGGTCGGGCCACAGACCTGTTTCTTCTTCTTCTTCAGAATAGGCATGTGCTACTTCTGGCTTGSTGATGAA[A/T]CTTAGGTTTATCGTGGAGATGGTACAGAACTATTAGCTATAGATATCTGGGCAATCGAAAACTGTTTTTGTTTCTGTTAGCTATAKAGGCGAAA	SEQ ID NO:127
PHM2100.21	GAAGGGGGGGGCCCGGAGNAAATTWCTYYCCSSSSGGGWAWWWAWCWWWAWARARADHHHHMMMVRNVSCRRRRRDRRMHMHNVBSNDRDDNNBNNNNNNHWWADDNBSSCC------TTTTT-------GB-BTK-G-SCYWW-TYY--M--CC-Y-H---A-A-W-C--AG---AW-W-TW-M-CY--SKH-HBGRYYYDWY-YH-WAM--AWWT-TTTT---WAAAA-TKAGKT--A-CG-AWA-RRGG-----YYYW-AADAWKGC-DTWACCMGTYTWAAAA-AS-GTCMGAAYCMY-TCC-M-GGCCYTT-BG-GAAMMMCKRG-GTAAAAGGTTYRAAYCGRKGCBNADATWA-ATT-CAHGATCRNAWVAA-NRKRWT----TACTTTK--TMRRKSMRBGC-TAHTYGTYMA-GTCMGRGRA-TGACAGBTH-SHWHCCAATY--GCAWMATCTKGTTYTRKGGDG-AYGTYGYKCTGAWRTRT--CTGCCCKCTTCT-CGACAGATAGTAGAGGAAGCTGGTGGGGTGGTAACTCGCATGGAYGGTGGAGAGTTTACGGTCTTCGATCGCTCTGTTCYTGKTTCCAACGGACTTGKTCATGGACAGGTTTGTTTGTTGT[C/G]AACAATTTGGCATATT-GTTTGTGGYKTTCATGGACAGGTTTTGTTCTTAGTGTTGTCTGTG-TGGACAGCTTTTGGAYCGGATCGGCCCTCCTACTGAAGACCTTAAGAAGAAAGGGATCGACTTCTCGTTGTGGTTCAAGCCTGACAA-TACCCKACYGACTTTTGAGC-GCAYCAAGG--------CA-------CCACCACCAGCCATKGCCACCATAATAAA-GCAGCCATCATTTKKDRRRVM	SEQ ID NO:128
PZA00521.3	ARTTCCCATGAAAAAGGAGACCRGKATGCTTTTGTATCAATGCTTGAGGCACTATGCAATGCAGAAAAGACAACAGAGGCTATTGATCTACTGCATATGATGCCTGAAAAGGGGATTACTACAGATGTTGGAATGTATAATATGAT[A/C]TTTTCTGCTCTTGCGAAGCTGAAGCAGGTGTCTTTCATGAGCAGCCTCTATGATACGATGAGAGCCAATGGTGTTGTTCCTGATGTTTTCACGTA	SEQ ID NO:129
PHM5599.20	AAAAAAAGYGSAGDVVKRRKRMBDWGBYMNNKMRRAMRVRRAAVVNNDDNNRRRRDDNDNDDNNNDRVNRHDVRRRARADNCCVAR-TYMDRRM--K-ARVRRVGG-ATCCVG-TGCCGSSGVMRACCGG-TTYRAVGCYATCSGVACCSTBGTCCCGSG-SATGGTCAAGCTGGTGGMGGAMACMRCCGAMCAVGTYCWHSRNTTYGARGKKCC-GGAGATGATAGAGAGTAAGCTAGCTAG--SAMRCRM--TBRWYTYAGGA-------MTGSWTGTWATCTWAATCTTAAAAAA-----ATSATTTGCTTTGCYAGGGGACCGGTTCKCGTGGTTCAARGACGARGAGTTCGCGAGGCAGACGATCGCGGGGCTMAACCCGCTGTGCATCCAGCTGCTGAC[C/T]GAGTTCCCCATCAAGAGCAAGCTGGACCCGGAGGTGTACCGGCCAGCRCAGTCCGCCATCACCAAGCAGATCCTGGAGAACC-AGATGAAC-CGCSCGYTCACCSTGGAGCAGGCGCTGGCGGCGAAGCGGCTGTTCATCCTGGACTACCACGACCTGTTCCTGCCCTACGTGCACAAGGTGCGG-AGCTGCAGGACKCGACGCTCTACGCCTSSSGCACCRTCT-CTTCSTGACG-R--MCBK-YAC--KDBSHHDNBSGKKDWA	SEQ ID NO:130
PZA00193.2	ACTTTMCRGGCCACACCAATTCTGCTTGGTTCTTGAAGATACATTCTTCCTATGGTGCCMCCTATATAAAAGCCATTTCTGG---TTATGTTTATCCTTGACATGTCAACAGAT[C/T]AGTGTTGGGTTGCAGTCATGCGGTCCTTAAGTCYMGGAGAAGGCGAGAAGTCATTGCTKCTAGCATTGTGATCGTCGGCCAC--AAGTAATCWAAAAGTGACAGCTACTTGTTCCTAGCAAATGGAGAAGGGCGATATATAGGTTKATGATCAAATTCAGT--------GTATGCAAGCAGCATATTTTGTTTAGAGWTAGCTTT	SEQ ID NO:131
PZA00445.22	ACAACCTACTAGCGTCATGTTCTTT----------TTTTYTTCTTCTT---TCCCTTACAATCCCTTAGTTCTTGCAAGCA-CAGCTGTACATATAASTAA[A/T]TTCTGGTGATTGACTGATCTTCTTTKTTCTGGCAAACAAYTGCAGGCCGCACAAGCTTCAGGCCGTGTGCAAAAGTGGGGCGGCAAAGGCACCGATGAAGT	SEQ ID NO:132

Figure 5B

Marker Name	**Context Seq**	**SEQ ID NO:**
PZA02151.3	GTCCACAGRGGAAGGAGAGGTGGGTACAACAAGAGTCCTGTACGGAGCCGTTCACCCCCCGCCAGGAAAAGGTCACMTAGCGATCGTGCACGGTCAGTTTC[C/T]AGGAGCCACCTTTCTAGGTCAGTATCAAAGTCTCCACCAGTGCATCATCCCTCSCCACTTGATTCTCCATCTCTGGAGCGTGCAAGTGATGG-AAATCTCG	SEQ ID NO:133
PHM15427.11	ANANNNNNANTANGGARAARAATMWKGGRR-A-G-YTTTKR-A-DRA-B-SG--WW-RG-TT-W-RG-G-GGNA-HA-MA---AYY-AA-MGG-TWGGAT---CAA-A-GA-MRAHWGGG-KTA-CC-MGG-RA-CGGGG-RGKTTYTTGG-SATTTT-TGTYTG--SAA-HHA-MTTYTGMAAGCYTGCCCAGGGGTTAMTTTYTCCTGKTAT-SGVACCGAAAGCSCGKCAMGACGACGGCAGCCTGGACCTGATTCTCGTCCATGGAAGCGGCAGGYTGAGACTGTTTTGSTTCYTTGTTGCCTATCAGYTCTGCTGGCATCTTCTRCTCCCCTACGTGGAATATGTCAAGGTATGTATCGTGACTTTCTTTGTATCTGTTTACAGCGCTTGTTGCGGCGGTTCATGTACCTATAGGGCTTA------------GTAGATATCCTTGACCTTAGTAGCATGCTCTTTCCTAGAACA[C/T]AGGACTCCATCAGTTTGTCWTCGCTTCTTAGATGMCCGTGCACTGATGTGGYATTTTGTTGTTGCGRCAATGATT-GCTCGCAGATAAAAGAAGTGAAGGTTAGGCCAGTTGGCAGTACCCACAGTGGTTGTGGYGTCGACGGTGAGCTTCTKGATGGAGAGSGCGGTGCTGAATGGCAGTGCTCGCTGCTTCCAGMAC-AAGGCAGGCTGCTTG-CMR-G-ATCC-B--GK-SY--RVB-NNRNKKKGAAARAAAA	SEQ ID NO:134
PZA00521.3	ARTTCCCATGAAAAAGGAGACCRGKATGCTTTTGTATCAATGCTTGAGGCACTATGCAATGCAGAAAAGACAACAGAGGCTATTGATCTACTGCATATGATGCCTGAAAAGGGGATTACTACAGATGTTGGAATGTATAATATGAT[A/C]TTTTCTGCTCTTGGGAAGCTGAAGCAGGTGTCTTTCATGAGCAGCCTCTATGATACGATGAGAGCCAATGGTGTTGTTCCTGATGTTTTCACGTA	SEQ ID NO:135
PZA02207.1	TBSSSSYTCACTAAGTGTGATTGTAACAGTGGTACCTCTTGTGTTCTGTGTTCCGCGATGTTGCAGTTGGTTGCTTGATCGAAAGATGTTTCA[A/G]CCTCCCATCTGCTAGCTATGATACAGATGGTYCCTGATAATAATGATGACATATTCTGTGATGGATGCCACRRCATTTTTTKKTTTTGTTTTTGCATTCAGATATTTCRGCTTCCTKRTAGTTTTACATGTCCCAACTAGGAATGAGAAC	SEQ ID NO:136
PHM565.31	TTKVNNBN-----W-HM-AVR----CTGAAGA-TTGCTGAAGGAGTGGGAGTCTAGC-AAA--YY-W-----TTCCGTGTCCCAAACGTCCTGCTCACAGGGTACCGCCAGAAGGCCTTGCTGGACA[A/G]GGCCGAGATGCTGCTCGACGGCTTCTTGAAGAAGGGAAAGACGCCTCCTTCGACCAGCTGGGGGATYGTGGCAATCGGCTATGCGGAGAAAGGTGATGTGGCGAAAGCTTATGAGATGACCAAGAACGCCCTCTCTGTGCACGCCCCCAATACTGGCTGGATCCCTAGGCCTTCCATGCTTGAGATGATACTTAAGTACYTCGGAGACGAGGGGGAGGTCAAKGATGKHKAAGCTTKCGTTAGTCWGCT----GAAAGCTGCTGTGCCASTGGACTCTGATATGACCGAGGCTTTGTCKAGGGCTCK------TKCSAGGGAADAAAKGAWKGCTR---AARAGGCARCGGAAKCTCCTCGCGGGGATBWTATTGCCTRARCTBGYWKTCSGTKTTT-CASCGCTKC-KYCYVAAWKG--TC-W-NYTBWNNNHYHCRADHBDNBBNNHNNBNNNYNHNNHNVNNNNNYNBHHNKBRYYYNCTNTTNNCGCNA	SEQ ID NO:137
PZA03578.1	ATGCAGCAGAGAATACTGTGGAAGKTGAYGATAAGAAAGAGGAAGCCCCWGCTGTNGATGCAGCAGAGAAGAAYGAGGAAGGTGATGATAAGAAAGAGGAGGAGCCCCCTGCAGAGAA[A/G]ACTGTTGAGAAAGAGGTGGTCCCTGCTGTAGATGCAGCAGAGAATACTGAACAAAGCACCGGTGGGCAAGCACAGCCTAAYGATGTTGSTGCCCCA	SEQ ID NO:138

Figure 5C

Marker Name	Context Seq	SEQ ID NO:
PZA00300.14	AAAAAA-- TCCTCTTGTCTATCCGACRCCMAAACATAGGTCTAAGGTCYRSTTTYGRTYGYGKTCGTTC- TMACRTGRGCTACRRTRCCRYTGTGTATKGACATATGTCTCAARCYTAGTTTTCGTYRTGGTCKATCTC TCATCKGTTACRSTTTTAC-GCTAYCTA--------TGGGTGACAGTSKAASMSTCTAASGGTTTTRTT- -------GWG- AAGWTTTTTTCTTAATACAATACWYNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAGGRGTTRTCTTAGC CYWCAGGTCATTTTKTT- ACMGTCTGAATTTCTTAYACTTTYTAGGTCAGTAGTAACTTGTAGATTTYGACTTGATTTTCACAGGCC TGATTAATGCATTGAARYTTATCCARCMKATCAARGACAAATACMCAGGTAYCACTTATGCAGATTTGT TCCAGTTAGCAAGTGCTACGGCGATTGAGGTCACTGTCCTTTCTCTGATTAAGTATCTGACTTGGTCAC TTKATCACTCAAGTCTATGYAGTCATATGTTTTGTCAATCACATGATACAGGAAGCTGGTGGTCCAAAA MTTCCAATGAAATATGGACGKGTTGATGTCACAGCAKCTGARCAGTCTCCRCCCGACGGGAGGCTTCCY GGTCAGTGTTTCYAATGGGTTCTTCATTCCATATCAATGTTTCATT[A/G]TTGTTTTGTTCAATG- CTTGCAATGTGAYTTATGAGAGGTGCCTATC	SEQ ID NO:139
PZA00067.10	GGGAACTGTAGTTGCAATTGGTAATTCCAGCATGCATTCCACAATRTCACAAAACAGCTAAACRTAAAT CTCTGTMTATAAGTGAGATACCAACATTTTTGCCTATTAATTTGCAGCTAGCAAATGCCTCCCCGGACC TCATCAACAGGCTGATCCCAGACCATGCTAGGCGGCATCTTGGGCTCACTTTATTGCCCACC[A/G]CT GGACCATAGGCGAAGGCTCTATGGTGTTTAAACCTTGCTCTTTCTGATTCTTCGTTGTGCCATAGGCAA TTCAAGGTGTAGAATCTGACCATTATTGGAAAGCCAAACACGAGCTGGCGCCAATGTGTTGCATAAGGA GAGGCGGTATGTTSGTGYAGCCAGCCTTTTGYCGCCTGTTTTAATGCAAAATCTGATTT	SEQ ID NO:140
PZA01563.1	AAAGACAGCTAATGTCCTGACGCGAAGTGATCTGCGAGCTCGCAGAAGAGGTCGCAGGCATCATCGGCA TGCTGATGACTAGTTTCCTATTGTGAATGTTG[G/T]GTAGAAGTGCTGTGGAATACCCWAGAC- ATTACCATTTTATTTGGGCCTCATGCCCC	SEQ ID NO:141
PZA00647.9	CGTTYGAGGYGGATCGTATCTGYCKGY----ACGCAGTGTTTGGSMAAA--------- TACTTGGGAGTCGCAAGAAAT---TGTGTAAATTAT-- AGA[A/G]GAGGATGGCGACGAAGCACGCATGTGTTACGTAGTTGGGGTTTGTGTGCACATGGTGGTGG GCAGGGK---------CTAG-------AGGGTTTATHTTTRGGTTATTTTCSYAGTGGAATGWATCTTA	SEQ ID NO:142
PZA01005.1	TTGTGGTCTTGGGAGTYGGACTTTGATTTCAAGGCGRAGCAAAATCTTRCAGAGATGGCTGAGGAACTG CCTCATCTGTAGCCTGTTTCTTAAAATAATGT[C/T]CAGTTTCTTTACTTGCCTGTAGCCTCTATAAG	SEQ ID NO:143

Figure 5D

Genotype	lsmean_akw	lsmean_cd	lsmean_cl	lsmean_cw	lsmean_kc	lsmean_krn	lsmean_kw	lsmean_sdw
B73	0.2595	27.1442	137.4	22.9893	362.29	17.1534	92.6875	0.1017
B73xM0001	0.3101	28.1164	181.28	33.8449	584.33	17.463	181.5	0.1049
B73xM0002	0.2679	26.4717	163.18	27.4389	607	15.9049	161.5	0.1116
B73xM0004	0.3237	27.8184	179.57	32.5551	593.16	15.7855	192.4	0.1194
B73xM0005	0.3312	24.9233	167.28	20.9466	454.08	13.9758	148.87	0.1085
B73xM0006	0.2748	25.5387	195.95	27.959	679.77	16.9334	187.92	0.0882
B73xM0007	0.377	27.8707	234.14	41.6269	797.84	15.3992	299.18	0.1334
B73xM0008	0.3225	28.7335	171.83	33.3876	608.43	16.2448	196.87	0.1059
B73xM0010	0.2719	24.9718	166.44	21.6692	588.72	17.2854	158.64	0.1201
B73xM0011	0.3265	29.7292	173.29	36.7821	615.85	16.2761	200.31	0.1303
B73xM0012	0.3045	29.7283	210.41	35.6542	661.18	15.4226	201.68	0.1143
B73xM0013	0.2773	26.9557	171.75	28.8212	591.29	16.8877	163.3	0.1223
B73xM0014	0.2633	26.2687	167.46	25.9295	558.84	16.0012	145.88	0.1419
B73xM0015	0.3443	28.3233	182.58	33.3802	583.4	16.7054	205.19	0.115
B73xM0016	0.2814	29.974	186.04	30.4703	659.37	17.5389	182.22	0.08767
B73xM0017	0.3084	27.6901	183.9	36.6454	656.43	17.3747	201.69	0.1368
B73xM0021	0.2478	26.7921	173.18	27.9359	607.05	16.4917	152.03	0.1264
B73xM0022	0.3122	27.9593	158.47	31.1828	497.24	17.3587	153.55	0.1408
B73xM0023	0.3453	26.4406	199.84	33.3168	641.09	15.7028	217.09	0.1068
B73xM0024	0.3354	26.3232	191.37	28.8058	482.32	15.2159	153.55	0.1241
B73xM0025	0.3028	29.6752	190.91	40.2341	567.79	16.9306	171.45	0.1266
B73xM0026	0.3249	27.6211	183.27	37.2246	545.28	15.8354	174.72	0.107
B73xM0027	0.3286	26.435	194.1	30.4513	592.75	15.1728	195.48	0.1227
B73xM0028	0.2783	26.6366	169.89	25.3544	577.48	15.9628	155.77	0.1012
B73xM0029	0.2908	26.4605	179.54	28.6736	640.68	16.4532	184.07	0.1137
B73xM0030	0.271	25.8424	169.78	29.9544	512.13	17.1311	153.4	0.1009
B73xM0031	0.3026	27.0307	175.82	29.882	570.2	15.3025	170.5	0.1432
B73xM0032	0.3555	26.3289	176.4	28.2879	531.45	14.4228	183.09	0.1337
B73xM0033	0.2949	27.2646	158.08	24.8191	440.75	15.3438	131.76	0.1015
B73xM0034	0.2805	28.5391	157.66	29.1271	620.44	18.178	174.71	0.1372
B73xM0035	0.3149	26.2485	180.37	26.9169	505.83	14.8047	156.68	0.118
B73xM0039	0.3108	28.8997	179.31	33.6196	677.77	17.3061	209	0.1122
B73xM0043	0.322	26.6904	193.78	28.0799	511.55	15.5254	162.64	0.1127
B73xM0044	0.307	27.198	189.59	30.9399	606.45	15.7789	185.3	0.1224
B73xM0045	0.295	28.1607	183.67	30.9309	704.58	17.2086	206.12	0.1326
B73xM0046	0.2676	26.206	171.16	28.811	563.65	16.4189	153.18	0.1043
B73xM0047	0.3019	24.929	191.78	25.0654	583.08	16.032	173.8	0.1166
B73xM0048	0.2886	26.1159	182.1	27.4087	449.74	14.7765	137.67	0.12
B73xM0051	0.3098	25.432	164.5	24.4078	459.16	15.9868	144.89	0.1372
B73xM0052	0.2849	26.8314	157.48	26.542	494.21	16.5933	137.95	0.148
B73xM0053	0.3164	28.1179	157.33	25.7426	503.87	16.89	156.26	0.1039
B73xM0054	0.2818	28.4499	163.08	30.978	659.09	17.9552	188.03	0.146
B73xM0055	0.3107	30.2395	179.29	35.4068	623.64	17.5596	193.87	0.1269

Figure 6A

Genotype	lsmean_akw	lsmean_cd	lsmean_cl	lsmean_cw	lsmean_kc	lsmean_krn	lsmean_kw	lsmean_sdw
B73xM0056	0.2726	27.44	169.7	30.7976	660.03	17.4709	178.11	0.1212
B73xM0057	0.2981	27.1025	176.38	27.2853	578.86	16.2581	172.09	0.131
B73xM0058	0.2644	30.4467	182.44	33.9425	706.48	19.6622	183.47	0.1077
B73xM0059	0.304	29.3215	161.88	33.1415	630.57	16.7667	191.36	0.1267
B73xM0060	0.33	30.2356	179.79	35.9485	562.79	16.5075	185.17	0.117
B73xM0061	0.3071	26.9444	174	36.2395	584.67	16.0219	191	0.0738
B73xM0064	0.3365	26.7835	168.88	30.6917	531.33	15.7784	179.56	0.1153
B73xM0065	0.2818	28.784	175.47	27.7036	648.04	18.1512	180.73	0.1122
B73xM0066	0.1977	19.5575	101.53	7.8955	-7.859	NA	-2.0902	0.1138
B73xM0067	0.2961	29.1853	204.82	39.8805	708.79	16.2886	209.28	0.1191
B73xM0069	0.2666	27.0921	167.51	27.0508	567.19	15.7779	151.35	0.1357
B73xM0070	0.2847	24.6849	156	20.1382	440.55	14.8029	125.33	0.1124
B73xM0071	0.2518	27.404	152.48	24.9957	533.27	16.9949	132.29	0.1197
B73xM0075	0.3148	27.1813	189.12	33.566	579.03	15.5646	180.29	0.1148
B73xM0076	0.326	28.0846	187.86	34.9719	573.16	17.4676	179.23	0.09064
B73xM0077	0.3394	28.5536	210.3	39.366	748.98	16.917	254.95	0.1531
B73xM0078	0.3363	28.453	173.33	36.0084	540.19	16.8252	180.16	0.1127
B73xM0079	0.3059	24.8338	167.02	28.0315	487.36	14.9727	158.23	0.1103
B73xM0080	0.3197	26.9056	167.47	29.1389	544.13	15.7142	169.81	0.1167
B73xM0081	0.2885	26.4711	181.93	31.6459	639.01	15.906	184.36	0.0933
B73xM0083	0.3447	28.1369	167.53	29.9941	514.75	15.019	181.1	0.1405
B73xM0084	0.313	26.6476	187.76	28.44	590.23	15.7056	185.14	0.1015
B73xM0085	0.2824	25.0313	156.75	26.6963	517.35	16.7402	153.68	0.1375
B73xM0086	0.2917	25.7823	171.58	26.2372	574.63	16.9091	168.63	0.1439
B73xM0088	0.3115	28.5759	201.69	41.515	694.16	16.3236	216.87	0.1145
B73xM0090	0.3098	27.6035	183.2	29.7685	630.01	17.576	192.64	0.09848
B73xM0091	0.3121	28.3291	178.12	32.085	609.06	16.0602	190.49	0.1322
B73xM0092	0.3247	25.4252	181.72	24.6308	619.51	15.8535	202.11	0.1428
B73xM0093	0.2985	25.5809	201.04	29.3307	630.51	15.5789	188.07	0.1033
B73xM0095	0.3295	30.2535	176.39	34.3908	577.19	17.0787	183.57	NA
B73xM0096	0.3039	26.8474	182.05	31.5766	638.62	16.209	196.81	0.09762
B73xM0097	0.3131	26.3553	184.04	29.6558	588.29	15.1427	181.54	0.138
B73xM0098	0.2864	26.0877	186.39	28.1589	584.41	16.6328	166.19	0.122
B73xM0099	0.3451	27.9588	184.14	35.096	526.08	16.6067	176.12	0.1255
B73xM0100	0.2969	25.5007	173.56	28.7216	498.78	14.2774	148.09	0.129
B73xM0101	0.3319	28.0719	195.12	32.2307	633.99	16.0261	207.27	0.1098
B73xM0102	0.3367	NA	NA	38.0738	764.25	19.8722	257.27	0.09284
B73xM0103	0.322	26.9912	190.99	30.8157	619.81	15.5317	197.82	0.1166
B73xM0104	0.3101	28.144	165.88	27.3816	472.08	16.0363	142.66	0.1345
B73xM0105	0.3074	26.3984	182.52	32.885	595.71	16.1994	180.99	0.128
B73xM0106	0.3057	26.3683	174.39	27.528	509.12	16.5049	156.48	0.06513
B73xM0107	0.2691	26.998	181.44	31.5489	635.43	15.1491	169.26	0.1158
B73xM0109	0.3099	26.512	187.36	27.7666	573.02	15.5144	177.96	0.1034
B73xM0110	0.3312	28.4706	183.96	37.9613	614.11	16.9469	201.94	0.1092

Figure 6B

Genotype	lsmean_akw	lsmean_cd	lsmean_cl	lsmean_cw	lsmean_kc	lsmean_krn	lsmean_kw	lsmean_sdw
B73xM0113	0.2631	28.0617	147.66	24.2872	522.17	19.0758	129.31	0.09075
B73xM0114	0.2819	27.4205	188.22	32.8694	657.54	16.8195	188.59	0.1457
B73xM0115	0.315	28.2104	198.7	32.4641	626.89	16.0885	197.24	0.111
B73xM0116	0.3659	26.9832	174.11	28.5788	525.44	15.9639	188.8	0.08741
B73xM0117	0.3328	27.9861	222.29	38.3702	710.27	15.9627	236.5	0.1099
B73xM0118	0.3155	26.7717	187.11	30.9926	613.88	16.04	191.38	0.1212
B73xM0120	0.2979	28.3668	186.31	34.1538	718.07	18.8496	213.37	0.09768
B73xM0121	0.3079	26.6292	176.14	28.6534	564.71	17.1895	173.22	0.1096
B73xM0122	0.32	27.8995	157.31	28.6237	500.61	16.7833	169.2	0.1139
B73xM0123	0.3188	24.5946	195.09	24.4953	585.68	14.52	182.8	0.1028
B73xM0124	0.2723	27.3256	185.33	28.7176	634.18	17.1697	175.24	0.1297
B73xM0125	0.2448	29.1155	182.25	32.611	592.44	17.2059	139.09	0.09623
B73xM0126	0.3177	25.8731	190.89	30.197	543.73	14.8095	172.95	0.1037
B73xM0127	0.3136	26.9867	194.88	34.1478	629.78	15.7746	198.27	0.1244
B73xM0129	0.3249	29.2382	191.79	37.7068	619.71	16.24	201.9	0.1341
B73xM0130	0.2902	25.4749	167.24	26.0344	556.52	16.6732	151.39	0.09043
B73xM0131	0.3169	26.5891	191.42	30.0734	630.76	15.7303	201.22	0.1109
B73xM0132	0.3309	27.0813	186.08	30.8376	575.98	15.456	189.23	0.154
B73xM0133	0.3064	29.4285	180.77	34.3598	618.98	16.6212	190.3	0.1059
B73xM0138	0.2999	25.3037	159.97	22.4477	494.39	14.9309	148.85	0.1499
B73xM0141	0.3405	29.2962	182.49	34.2248	669.11	17.0368	226.13	0.08872
B73xM0142	0.2738	26.3302	165.36	25.2784	537.58	17.4188	151.5	0.1071
B73xM0143	0.2677	29.5453	175.04	32.1487	503.14	16.106	136.43	0.09557
B73xM0144	0.3152	28.0045	193.71	35.3415	638.48	15.9763	198.7	0.1227
B73xM0145	0.3163	29.4406	167.09	37.1712	525.83	19.2391	164.07	0.1212
B73xM0147	0.3128	26.6207	185.18	29.4473	598.73	15.5105	186.81	0.1337
B73xM0149	0.2646	26.862	170.61	29.3068	650.69	18.6618	170.5	0.1084
B73xM0150	0.2826	24.274	152.94	19.4662	466.23	16.0045	131.58	0.1258
B73xM0151	0.2876	29.4213	175.25	30.2844	686.51	18.0357	196.64	0.08479
B73xM0152	0.3118	26.252	169.55	32.0868	604.43	16.4573	181.5	0.08977
B73xM0154	0.3283	26.6253	190.29	34.3098	660.87	15.2626	212.24	0.1292
B73xM0155	0.3441	25.7286	199.14	33.0832	575.71	15.1614	197.62	0.1232
B73xM0156	0.3126	29.2853	169.76	29.9742	634.64	18.6352	197.1	0.1323
B73xM0157	0.2943	28.3187	198.38	33.2948	640.92	17.0086	187.26	0.1383
B73xM0160	0.2898	27.69	183.01	32.1438	653.34	17.5097	184.5	0.1012
B73xM0160A	0.3039	27.616	176.25	31.1063	605.55	16.9416	184	0.1268
B73xM0161	0.3356	26.3175	192.58	33.2661	520.99	15.2718	173.6	0.1163
B73xM0162	0.2825	27.4193	172.42	29.0666	631.94	16.3621	179.26	0.1161
B73xM0162A	0.267	27.0522	181.84	30.8981	608.23	17.8773	162.16	0.106
B73xM0163	0.2948	28.6792	189.36	34.2046	630.09	17.7311	184.38	0.1308
B73xM0165	0.3196	28.233	169.85	31.4613	614.87	17.8335	195.03	0.1051
B73xM0166	0.3099	25.2282	178.13	26.7965	486.18	14.6912	146.21	0.1286
B73xM0167	0.2557	27.6055	171.56	28.595	599.99	16.5939	148.92	0.1195
B73xM0168	0.3321	29.6078	180.13	38.515	599.18	18.208	193.58	0.1145

Figure 6C

Genotype	lsmean_ akw	lsmean_ cd	lsmean_ cl	lsmean_ cw	lsmean_ kc	lsmean_ krn	lsmean_ kw	lsmean_ sdw
B73xM0169	0.2861	28.5674	143.97	25.9357	298.58	19.1748	98.1504	0.1267
B73xM0173	0.3093	28.4041	174.61	31.3411	588.61	16.9158	180.59	0.1071
B73xM0174	0.3166	27.005	188.46	32.7953	513.58	15.1595	175.3	0.1202
B73xM0176	0.2945	27.4412	169.52	29.6208	591.51	17.157	174.82	0.1278
B73xM0177	0.3244	29.5096	204.83	38.1799	676.08	16.9821	218.12	0.1226
B73xM0178	0.2878	28.0398	175.46	32.3741	698.65	17.8257	201.85	0.09085
B73xM0179	0.3158	27.606	188.41	30.6407	608.75	15.3211	191.05	0.09952
B73xM0180	0.3216	26.2836	173.51	27.0455	563.59	16.2188	177.73	0.1146
B73xM0181	0.3025	29.7013	188.12	36.2445	679.71	17.9615	204.44	0.1116
B73xM0185	0.2897	26.5551	183.97	29.4089	638.06	17.1099	178.12	0.09866
B73xM0187	0.308	30.2933	174.41	32.7023	664.9	17.8709	204.18	0.13
B73xM0188	0.3052	29.8018	184.08	32.6425	543.22	17.4734	166.58	0.1051
B73xM0189	0.3583	28.6137	180.91	37.9238	648.7	17.8861	226.9	0.1055
B73xM0191	0.2928	26.4914	159.58	25.254	474.76	16.028	144.27	0.1158
B73xM0192	0.1919	30.6147	177.68	30.5342	594.31	16.9716	109.81	0.08821
B73xM0194	0.3092	31.343	189.1	38.9674	671.93	18.3769	209.09	0.1122
B73xM0195	0.3408	27.8783	178.19	35.3488	569.27	16.1932	187.07	0.1168
B73xM0196	0.3041	30.4218	181.28	38.9166	621.1	17.6845	186.13	0.1022
B73xM0197	0.2721	28.6628	165.7	33.1256	633.53	17.1766	172.65	0.0906
B73xM0198	0.3481	27.7774	176.04	29.7992	487.3	15.9418	155.42	0.1144
B73xM0199	0.2204	22.3869	136.49	17.7517	316.12	14.0975	96.6883	0.1256
B73xM0200	0.299	29.1341	196.89	36.6559	682.01	16.3888	200.86	0.1264
B73xM0201	0.3176	29.0577	182.74	35.1432	743.49	18.4306	233.66	0.134
B73xM0203	0.3201	28.6493	186.98	33.4681	625.2	16.6719	198.14	0.1067
B73xM0204	0.2932	26.9812	177.54	30.5402	636.78	15.4159	186.05	0.1125
B73xM0205	0.3572	28.2665	196.43	37.8177	602.81	15.5329	212.35	0.09405
B73xM0206	0.2936	25.692	169.72	26.6998	574.29	16.7344	171.75	0.1278
B73xM0208	0.2939	27.7785	172.52	31.6822	605.41	18.2061	183.21	0.09696
B73xM0209	0.2904	28.1787	161.05	29.1701	561.28	17.7977	163.46	0.1104
B73xM0210	0.3108	25.7738	202.59	31.896	559.35	14.6436	171.52	0.1257
B73xM0212	0.3332	27.0246	182.56	29.2342	546.35	15.8409	179.92	0.1343
B73xM0213	0.3208	28.6411	176.99	32.7619	573.55	16.3591	185.03	0.1407
B73xM0214	0.3004	24.2184	181.96	30.0479	584.97	16.1755	174.72	0.09616
B73xM0215	0.3265	27.2333	196.41	39.6021	590	16.2261	193.48	0.1203
B73xM0216	0.354	27.1316	203.19	36.9773	688.21	15.9652	245.52	0.1039
B73xM0217	0.2825	29.8416	165.31	31.5655	588.8	17.7785	171	0.09439
B73xM0218	0.2967	25.9891	173.08	24.9739	561.93	16.5515	163.71	0.1132
B73xM0219	0.305	27.7116	182.46	29.2788	552.09	16.9375	169.4	0.1325
B73xM0220	0.2965	28.5531	176.29	33.8104	607.53	17.4716	177.85	0.09807
B73xM0222	0.3034	26.8884	160.56	24.8886	531.79	17.37	160.74	0.1194
B73xM0223	0.3322	28.5284	177.47	35.9272	664.34	16.9506	219.29	0.08632
B73xM0225	0.2669	27.3046	185.89	34.241	579.71	16.3748	176.26	0.1073
B73xM0228	0.2945	28.0168	173.44	32.9117	630.76	18.7321	185.43	0.1193
B73xM0229	0.3228	30.4849	200.67	38.5825	764.85	18.4197	246.2	0.1388

Figure 6D

Genotype	lsmean_ akw	lsmean_ cd	lsmean_ cl	lsmean_ cw	lsmean_ kc	lsmean_ krn	lsmean_ kw	lsmean_ sdw
B73xM0230	0.3668	28.0962	188.16	33.4792	489.82	14.5989	176.45	0.1063
B73xM0232	0.3141	26.0748	154.64	25.9453	494.11	17.0384	162.26	0.127
B73xM0233	0.2636	28.4872	162.12	30.9101	562.54	17.2134	158.46	0.08534
B73xM0234	0.3118	28.0183	185.65	32.0446	622.29	18.0969	190.97	0.08974
B73xM0235	0.3043	25.9212	187.25	32.8105	656.68	16.7231	199.16	0.1247
B73xM0236	0.3022	27.3661	174.58	29.4525	566.44	14.8905	168.87	0.1243
B73xM0238	0.272	27.6211	166.6	29.339	610.45	16.795	162.3	0.1152
B73xM0239	0.2929	30.0731	175.8	33.6907	669.51	18.8774	192.01	NA
B73xM0240	0.2787	27.3529	169.25	27.2788	598.51	16.2298	169.3	0.1266
B73xM0241	0.2921	24.5989	159.58	27.9388	548.98	16.6296	160.82	0.1038
B73xM0244	0.3196	28.2959	179.92	31.8863	642.09	16.3704	204.24	NA
B73xM0245	0.3053	30.2612	188.72	39.5222	627.43	17.4212	189.29	0.09293
B73xM0248	0.3164	26.3011	195.27	29.291	647.83	15.6177	206.02	0.1314
B73xM0249	0.2792	26.6816	160.69	28.2975	541.86	17.1102	163.1	0.09816
B73xM0251	0.2874	26.9698	139.79	25.6891	513.82	16.1813	146.9	0.115
B73xM0252	0.2968	30.481	199.48	41.0691	695.16	18.2836	206.71	0.1196
B73xM0254	0.2531	26.1339	166.59	26.2152	569.91	16.613	142.01	0.1253
B73xM0256	0.3091	31.0268	176.11	33.0721	415.27	17.2537	129.57	0.1206
B73xM0257	0.303	27.4571	174.48	28.5497	603.66	15.9837	182.32	0.09769
B73xM0258	0.2965	24.3528	166.15	25.7634	525.07	16.6647	156.24	0.1204
B73xM0259	0.3485	28.6526	187.26	32.011	548.55	15.7289	190.45	0.1096
B73xM0260	0.3114	27.6235	194.47	35.0733	659.01	15.9405	203.46	0.08964
B73xM0262	0.314	27.4262	169.73	28.1044	522.46	15.9843	163.26	0.09149
B73xM0263	0.289	28.3065	176.05	33.2936	676.93	17.6601	193.94	0.09037
B73xM0264	0.2861	29.2003	177.13	32.146	636.64	17.6564	184.13	0.1247
B73xM0265	0.2796	27.3228	166.25	28.0337	605.04	17.9386	172.96	0.1253
B73xM0266	0.2905	27.8926	179.23	31.975	618.71	17.4505	178.95	0.1251
B73xM0267	0.3015	29.2958	202.2	40.2081	727.95	16.9919	218.64	0.1115
B73xM0269	0.2876	26.3881	176.71	27.1684	557.89	16.2276	157.94	0.1269
B73xM0270	0.3255	29.0163	188.79	41.6554	601.44	16.3318	197.27	0.1256
B73xM0271	0.3165	26.7932	175.57	27.5189	542.57	15.1669	173.63	0.1084
B73xM0272	0.3237	28.2605	187.85	33.9213	664.94	18.7518	213.79	0.1175
B73xM0273	0.2787	29.4772	173.91	36.9312	670.14	18.4207	183.73	0.1122
B73xM0274	0.2798	27.5994	174.88	27.683	675.71	17.5946	189.52	0.09043
B73xM0275	0.2874	30.9402	166.28	30.063	526.94	18.2897	147.02	0.1046
B73xM0276	0.3236	27.6156	196.87	33.7596	668.55	16.2491	214.31	0.1023
B73xM0279	0.2861	26.778	165.02	27.6829	583.08	17.4188	165.4	0.1411
B73xM0280	0.3191	27.7502	181.72	30.3711	601.58	16.4054	191.74	0.1006
B73xM0281	0.3379	27.0304	150.14	22.2799	323.55	17.1157	108.76	0.106
B73xM0282	0.3071	26.8986	168.7	31.1155	521.61	15.8447	161.27	0.1282
B73xM0283	0.3542	25.5225	188.49	30.2171	428.17	16.1189	151.66	0.125
B73xM0284	0.3127	29.2253	204.36	35.1915	705.23	17.1835	220.57	0.1186
B73xM0285	0.2916	25.0723	183.23	28.3587	509.45	14.2553	154.31	0.1092
B73xM0286	0.3114	29.4138	183.93	38.4638	535.11	15.1666	166.54	0.1374

Figure 6E

Genotype	lsmean_ akw	lsmean_ cd	lsmean_ cl	lsmean_ cw	lsmean_ kc	lsmean_ krn	lsmean_ kw	lsmean_ sdw
B73xM0287	0.3156	28.4011	170.4	33.6796	586.69	17.8622	185.11	0.1096
B73xM0288	0.3205	28.4301	167.56	34.1142	659.78	18.3706	211.57	0.1292
B73xM0289	0.2927	25.4203	169.28	27.8567	604.27	15.6306	178.14	0.1449
B73xM0290	0.3128	26.95	150.09	23.5011	450.39	17.1814	138.08	0.1181
B73xM0291	0.2904	26.8935	174.32	26.5837	571.88	17.6587	164.89	0.1357
B73xM0292	0.3541	25.4321	189.04	27.4875	545.89	14.3447	194.04	0.1343
B73xM0293	0.332	27.8462	174.76	32.9004	580.58	14.9103	189.54	0.1198
B73xM0294	0.2886	26.1008	161.07	29.3327	601.29	16.0655	172.58	0.07219
B73xM0295	0.2958	25.7176	187.32	29.3254	627.99	16.3319	184.45	0.1497
B73xM0296	0.3296	29.6499	197.73	41.5882	714.4	16.4873	235.34	0.1141
B73xM0297	0.3115	29.6846	185.56	37.5406	678.79	18.0173	209.86	0.1246
B73xM0298	0.2674	28.4756	144.28	26.2476	599.79	17.6553	159.7	0.1121
B73xM0300	0.3277	28.5257	162.44	32.7923	472.58	16.0213	156.81	0.1163
B73xM0303	0.3453	28.9924	210.22	38.6097	662.23	16.0191	228.29	0.09598
B73xM0304	0.3393	28.4259	180.39	34.1712	564.36	16.6809	191.43	0.1016
B73xM0305	0.3308	25.5716	180.22	29.7927	416.48	15.0709	139.39	0.1372
B73xM0306	0.288	25.3048	120.48	31.6436	656.03	17.2622	190.64	0.1089
B73xM0307	0.3044	28.3113	193.98	37.794	614.92	17.2148	186.35	0.1078
B73xM0308	0.3464	26.5989	166.73	28.3454	573.97	16.2614	199.53	0.1139
B73xM0309	0.316	25.9622	151.41	25.5766	476.56	17.2043	145.78	0.1097
B73xM0310	0.2736	28.4564	175.71	32.4487	706.84	19.7402	195.29	0.1224
B73xM0311	0.3359	22.938	145.64	23.9016	489.35	16.6497	154.2	0.1116
B73xM0312	0.3039	26.3835	190.63	34.5391	609.14	15.7697	181.9	0.1047
B73xM0313	0.3155	28.067	183.68	34.3448	675.12	15.9796	212.27	0.1475
B73xM0317	0.297	26.3297	179.5	29.5773	578.46	15.3277	171.85	0.1177
B73xM0318	0.264	26.5524	177.43	29.2277	661.98	16.5675	175.94	0.07965
B73xM0320	0.3086	27.9755	181.56	31.979	602.49	16.7481	175.29	0.1123
B73xM0321	0.303	28.0633	177.1	30.3868	588.67	18.203	177.95	0.1147
B73xM0322	0.2641	26.8987	155.51	27.7175	624.02	18.186	169.18	0.1191
B73xM0323	0.3226	28.8635	204.61	37.6709	750.13	16.1337	241.52	0.1686
B73xM0324	0.3243	25.8175	167.44	24.6401	521.89	15.202	163.52	0.09345
B73xM0325	0.303	28.4093	190.48	31.9898	548.66	16.9407	155.25	0.1031
B73xM0326	0.2602	25.5118	172.47	28.2531	581.39	16.3532	157.32	0.1314
B73xM0327	0.3232	26.5656	207.55	32.9789	647.05	16.2672	209.13	0.1341
B73xM0328	0.2807	26.7385	178.87	31.5235	515.26	16.4145	161.04	0.1177
B73xM0331	0.2931	26.5482	154.26	24.8157	531.58	16.897	155.89	0.08251
B73xM0334	0.2312	27.3706	161	26.6431	635.38	17.2383	145.39	0.1012
B73xM0335	0.3283	26.3083	179.7	29.3152	575.77	15.2975	179.46	0.1295
B73xM0337	0.3308	28.6967	196.29	39.0613	615.87	15.9681	204.1	0.1327
B73xM0338	0.2721	28.031	180.07	34.1153	663.25	15.7455	181.71	0.1191
B73xM0339	0.2995	28.2237	176.54	28.2815	613.84	18.1075	180.64	0.08517
B73xM0341	0.3036	30.6689	196.33	37.5288	659.5	18.5023	198.94	0.117
B73xM0342	0.3096	24.6891	173.12	30.9744	616.93	17.538	190.4	0.1246
B73xM0344	0.3172	26.3924	187.08	29.4612	552.66	14.83	172.13	0.09646

Figure 6F

Genotype	lsmean_akw	lsmean_cd	lsmean_cl	lsmean_cw	lsmean_kc	lsmean_krn	lsmean_kw	lsmean_sdw
B73xM0345	0.3171	26.5061	180.28	27.9696	509.05	15.1169	150.99	0.1221
B73xM0348	0.2949	27.4685	182.04	34.795	620.2	16.2616	193.73	0.1025
B73xM0350	0.3087	24.7334	174.95	25.0974	538.36	15.0196	165.16	0.1263
B73xM0351	0.3344	25.7401	161.73	25.3787	511.76	15.4151	166.74	0.09494
B73xM0352	0.2761	27.0146	183.03	27.4947	647.76	17.9662	178.02	0.1377
B73xM0353	0.2759	25.7559	174.44	24.265	577.88	16.4364	159.06	0.1337
B73xM0354	0.2996	23.7637	161.05	27.4284	551.4	15.6671	164.01	0.09784
B73xM0355	0.3045	25.6376	156.57	23.3659	494.54	15.4797	149.72	0.1124
B73xM0357	0.2847	26.6383	167.05	26.5775	546.6	16.3968	157.48	0.1305
B73xM0358	0.2506	27.9086	179.9	31.9582	636.3	17.2415	159.21	0.08422
B73xM0360	0.293	24.0473	185.76	29.2956	550.98	14.9053	158.23	0.09992
B73xM0362	0.3005	26.1695	163.21	29.7265	537.07	16.6026	159.82	0.1495
B73xM0364	0.2812	27.1628	154.68	24.2533	437.7	16.2855	124.95	0.1232
B73xM0365	0.3077	28.8343	172.89	33.4321	614.01	17.8366	189.45	0.1183
B73xM0366	0.2815	25.5312	159.38	24.765	540.27	15.7475	145.9	0.1349
B73xM0368	0.2974	29.1424	189.46	36.5461	502.19	16.6059	146.7	0.1053
B73xM0369	0.2982	26.9479	188.99	28.4609	561.94	15.8003	160.98	0.09845
B73xM0370	0.2943	26.535	150.9	28.1706	468.55	18.1333	148.19	0.1441
B73xM0375	0.3103	25.105	160.52	24.7678	480.94	15.6649	150.61	0.1376
B73xM0376	0.3209	26.8237	196.17	31.8807	633.89	15.9095	204.26	0.1069
B73xM0377	0.2961	28.782	173.5	33.2581	600.24	17.6525	175.97	0.09691
B73xM0378	0.2748	24.8664	167.12	22.5344	580.63	16.1552	159.78	0.1111
B73xM0379	0.2994	26.5627	183.48	27.9675	570.66	15.2963	166.89	0.1642
B73xM0380	0.2986	27.2429	180.67	34.0894	530.04	16.3736	157.47	0.09916
B73xM0381	0.3144	26.38	178.45	30.8369	635.15	16.2874	198.69	0.1139
B73xM0382	0.2981	26.9467	169.29	29.7514	613.99	17.2047	182.3	0.1213
B73xM0383	0.3071	27.6232	169.31	32.8994	514.14	16.9241	154.08	0.1424
B73xM0384	0.3322	27.328	186.6	29.0853	570.97	15.8102	189.97	0.1282
B73xMo17	0.3686	27.0825	218.9	37.6859	715.1	15.5183	263.34	0.1409
M0001	0.2859	26.5275	163.4	29.3037	379.59	15.8634	107.61	0.1027
M0002	0.2535	25.0224	174.59	21.9656	509.12	15.5334	128.28	0.08098
M0004	0.2617	24.2016	142.61	16.7577	237.9	12.6328	57.7351	0.08767
M0005	0.2973	22.524	156.19	11.7494	256.15	11.0841	75.1675	0.1015
M0006	0.2344	22.167	169.66	13.4622	333.52	13.1674	80.1671	0.1104
M0007	0.3274	21.8922	179.16	16.291	270.83	11.4289	92.3018	0.12
M0008	0.2981	25.7724	158.15	20.9296	410.53	14.5868	128.81	0.1113
M0010	0.248	21.8552	150.65	12.8625	401.88	16.3409	99.0361	0.1137
M0011	0.2364	26.9029	132.66	25.7646	420.65	16.1073	99.5633	0.1061
M0012	0.2504	26.5836	183.84	23.4692	447.7	14.2122	113.1	0.1027
M0013	0.2308	24.4488	136.25	13.716	202.45	15.7473	44.6255	0.08065
M0014	0.189	22.5688	125.25	13.1924	363.49	15.2973	64.5322	0.09663
M0015	0.2778	23.3693	137.51	17.8851	221.44	13.8522	76.0938	0.07359
M0016	0.287	26.3089	153.02	16.006	281.26	14.055	87.0992	0.1122
M0017	0.2203	23.9912	151.12	21.4237	337.63	13.9718	72.343	0.1021

Figure 6G

Genotype	lsmean_akw	lsmean_cd	lsmean_cl	lsmean_cw	lsmean_kc	lsmean_krn	lsmean_kw	lsmean_sdw
M0021	0.2591	23.3531	161.65	18.3707	310.83	12.651	79.6367	0.08191
M0022	0.2908	24.4618	131.67	20.8886	229.81	14.2061	73.2903	0.1173
M0023	0.317	21.2198	129.33	10.2025	151.54	12.9122	49.0459	0.07695
M0024	0.2994	22.6154	164.18	14.3621	212.98	11.7631	62.376	0.109
M0025	0.2839	27.8531	158.63	27.7675	352.28	15.4104	101.68	0.1129
M0026	0.3254	25.2948	166.7	29.612	247.25	12.2086	82.335	0.103
M0027	0.201	23.6633	182.5	17.1417	301.5	11.4391	59.9703	0.09554
M0028	0.2016	22.4483	175	15.0644	306.13	11.1023	58.9192	0.0707
M0029	0.2561	24.3689	143.09	14.966	383	14.2288	97.4808	0.09568
M0030	0.2463	27.1007	184.48	32.7004	378.52	15.0975	92.871	0.1085
M0031	0.3142	24.6644	173.57	20.6894	403.92	13.3859	125.47	0.09347
M0032	0.1884	19.7639	127.16	9.9865	177.43	12.6192	42.3785	0.08764
M0033	0.263	24.9977	154.32	16.3065	402.51	14.065	99.1056	0.1011
M0034	0.2501	26.3464	127.94	17.1388	429.21	17.6376	106.42	0.1171
M0035	0.2013	23.2198	173.65	16.5518	354.56	11.8229	73.8062	0.09063
M0039	0.2991	26.2617	149.39	18.6744	296.07	13.5751	88.2861	0.1062
M0043	0.2678	22.9382	157.7	15.7541	210.29	13.4957	60.7891	0.1175
M0044	0.2713	23.8873	148.08	15.2996	258.95	13.2594	72.6319	0.06983
M0045	0.2998	24.4906	148.08	15.7007	256.98	16.0163	71.5428	0.08854
M0046	0.2292	22.3172	159.87	18.6989	285.67	13.0815	62.2995	0.09217
M0047	0.1725	17.6566	106.83	4.7874	180.41	11.8448	29.9731	0.113
M0048	0.2751	21.9637	154.91	16.9762	250.68	12.7007	68.9864	0.09831
M0051	0.2924	21.1691	150.77	14.6791	213.88	13.0475	64.495	0.1175
M0052	0.2919	24.7592	131.2	16.4113	309.05	15.5298	90.0123	0.09701
M0053	0.2234	24.5264	140.18	15.8915	293.79	14.0032	64.7039	0.1103
M0054	0.2924	22.1781	114.74	12.8988	229.46	13.4909	69.6237	0.09956
M0055	0.3094	22.6914	118.72	11.3372	87.883	12.0184	26.9349	0.07699
M0056	0.2716	25.0242	151.81	23.6113	421.64	16.9971	104.04	0.07624
M0057	0.2472	22.4621	148.09	11.635	131.18	12.5645	45.4588	0.1193
M0058	0.1895	28.5992	157.97	23.6896	579.43	18.9307	107.7	0.06974
M0059	0.2951	25.3905	124.03	18.5968	304.39	13.9891	84.486	0.09486
M0060	0.2687	29.0303	139.37	25.0916	285.59	13.6876	77.2252	0.1335
M0061	0.2931	23.3281	150.26	17.7468	270.05	13.3633	78.424	0.0718
M0064	0.1964	18.934	90.8285	11.1326	84.7267	14.4195	23.74	0.09375
M0065	0.2395	25.725	132.19	14.0144	407.73	16.8639	95.3189	0.1093
M0066	0.274	28.3675	179.49	31.2097	645.37	18.0649	178.17	0.08598
M0067	0.2827	24.4983	163.48	18.9464	248.02	13.5463	69.6642	0.1101
M0069	0.2685	22.6097	169.03	17.0964	114.05	14.7572	27.4481	0.09321
M0070	0.2418	23.0781	96.6753	6.0304	92.2261	NA	20.2684	0.08316
M0071	0.2683	23.2672	123.56	12.71	215.34	13.8038	58.3381	0.1072
M0075	0.2829	22.8851	134.98	16.2545	198.63	11.9685	55.2764	0.09211
M0076	0.3214	28.0786	206.15	37.8131	321.8	15.756	102.75	0.09477
M0077	0.3046	24.1432	173.32	23.7306	358.1	13.1668	106.73	0.09136
M0078	0.3368	21.5595	98.2741	4.0161	32.9997	NA	8.4501	0.09814

Figure 6H

Genotype	lsmean_akw	lsmean_cd	lsmean_cl	lsmean_cw	lsmean_kc	lsmean_krn	lsmean_kw	lsmean_sdw
M0079	0.2593	21.3203	127.25	13.3125	198.24	11.8453	53.1082	0.08487
M0080	0.2893	25.128	132.27	17.8868	224.63	13.8179	63.3734	0.07965
M0081	0.225	22.9089	142.39	15.9411	206.13	13.3675	50.2079	0.1173
M0084	0.3029	23.8157	174.44	18.9586	386.24	12.6672	116.57	0.08758
M0085	0.2353	22.1271	140.91	16.8698	283.86	14.2126	63.076	0.09788
M0086	0.2311	22.2386	133.06	12.4413	292.79	15.5366	68.6528	0.08611
M0088	0.3651	26.7438	181.11	33.1899	295.46	13.5644	102.85	0.1012
M0090	0.2182	24.2422	172.6	15.603	371.23	13.6735	78.8	0.08902
M0091	0.248	24.2236	133.17	15.2619	345.19	13.35	84.3987	0.1248
M0092	0.327	22.3842	131.36	9.6006	259.7	12.0058	84.4245	0.1048
M0093	0.2489	19.5396	160.55	11.1804	98.6319	11.5858	28.1707	0.09603
M0095	0.2661	25.3134	160.13	18.9746	313.39	14.9934	76.6449	NA
M0096	0.2436	22.5936	156.69	16.3384	300.39	13.4669	73.9812	0.08309
M0097	0.2924	24.5004	155.1	17.7738	287.4	15.1529	81.6988	0.1033
M0098	0.265	23.914	166.49	17.7438	370.01	14.2842	96.179	0.09784
M0099	0.2752	22.9851	141.52	13.451	75.3062	11.9508	15.0787	0.07973
M0100	0.247	22.5553	126.4	13.0866	201.88	11.2424	47.8065	0.08921
M0101	0.328	24.6646	168.52	13.8703	321.76	13.9883	93.0659	0.1018
M0102	0.2439	25.8265	169.42	20.6363	397.93	15.7764	96.9806	0.1102
M0103	0.3235	22.4454	157.61	16.4786	266.02	11.7772	84.7914	0.08916
M0104	0.3953	23.4777	107.29	11.4332	105.62	12.5131	43.5235	0.1129
M0105	0.2356	22.9109	123.63	14.6183	223.76	14.078	54.4597	0.08891
M0106	0.2869	22.3824	140.36	14.0748	232.79	12.85	69.9457	0.08323
M0107	0.286	23.8426	170.42	25.3622	362.95	12.2294	104.82	0.1095
M0109	0.296	22.3234	154.36	14.3532	318.64	12.7715	93.7282	0.07047
M0110	0.2557	24.0883	122.85	16.4222	211.39	14.1745	55.5573	0.09554
M0113	0.2774	24.7637	126.93	14.3011	347.7	17.7239	91.4469	0.09517
M0114	0.2202	23.4488	178.42	22.5342	430.37	16.1994	99.693	0.09644
M0115	0.2643	24.3116	161.61	15.6634	276.1	14.0072	72.382	0.0569
M0116	0.4229	24.1215	150.05	17.3071	221.26	12.2601	97.334	0.0927
M0117	0.2548	23.6879	167.1	21.3718	315.08	13.9294	79.321	0.07776
M0118	0.3094	23.4856	150.49	19.9839	298.45	13.4338	94.9023	0.1118
M0120	0.3077	24.1701	142.91	14.9383	235.31	14.7471	68.2765	0.1238
M0121	0.2947	23.2531	146.25	16.672	322.81	13.7735	92.5305	0.117
M0122	0.344	24.6905	143.1	22.2401	354.16	14.5509	120.63	0.1179
M0123	0.2666	20.3643	151.95	10.9315	307.01	12.5869	80.7945	0.0793
M0124	0.272	23.278	143.76	12.9637	277.16	13.6973	76.8582	0.09104
M0125	0.174	24.4815	192.44	20.4284	-0.5694	NA	1.9865	0.1068
M0126	0.2999	22.6849	174.64	16.1159	324.37	11.7972	95.3047	0.08604
M0127	0.3236	22.9376	151.38	18.5907	184.64	11.3945	59.9061	0.08265
M0129	0.2815	25.015	185.38	23.2868	348.99	12.3279	97.8501	0.07605
M0130	0.2764	22.3304	154.67	15.0958	277.4	15.721	72.9826	0.08454
M0131	0.2637	21.4115	137.38	9.3859	255.5	11.5356	68.1063	0.08768
M0132	0.2973	22.8792	145.24	16.0097	293.05	12.5047	86.6732	0.1057

Figure 6I

Genotype	lsmean_ akw	lsmean_ cd	lsmean_ cl	lsmean_ cw	lsmean_ kc	lsmean_ krn	lsmean_ kw	lsmean_ sdw
M0133	0.2355	26.8214	139.03	21.1535	430.95	15.751	101.23	0.07656
M0138	0.3069	21.8812	162.46	15.4647	341.85	11.6932	105.06	0.09558
M0141	0.3351	24.6348	147.08	16.7322	377.46	13.1313	127.77	0.08619
M0142	0.1914	22.6087	128.24	10.1443	221.6	15.1556	41.0717	0.07412
M0143	0.2904	27.7878	155.39	25.1203	272.4	14.1642	73.5285	0.1077
M0144	0.2534	26.4345	178.15	28.5502	439.72	14.9844	111.72	0.1035
M0145	0.3008	27.0389	147.48	22.8189	293.23	17.4392	89.1915	0.09915
M0147	0.2361	23.6199	142.72	13.7586	270.91	15.1489	54.9592	0.03079
M0149	0.2805	24.5003	158.25	17.73	344.97	16.3996	95.2594	0.08291
M0150	0.2624	20.7819	175.69	12.4784	326.96	11.9882	84.2676	0.08818
M0151	0.2796	22.5235	122.55	11.0079	191.06	14.6918	49.7656	0.1077
M0152	0.2856	23.6485	147.52	20.9886	218.67	13.7178	67.988	0.06919
M0154	0.2781	23.0956	160.65	20.322	386.24	13.0572	106.68	0.1148
M0155	0.3387	22.3971	162.54	16.1909	295.49	12.7174	100.48	0.09819
M0156	0.2676	25.966	147.54	18.976	420.79	16.2135	112.57	0.1003
M0157	0.221	25.4242	178	20.9785	501.17	15.0965	108.48	0.08377
M0160	0.2578	24.4973	168.56	20.1651	349.07	14.9743	88.1645	0.1442
M0160A	0.234	22.7732	104.3	10.293	107.26	14.4948	28.3732	0.1049
M0161	0.3	24.5162	177.06	25.364	394.93	13.2466	116.72	0.1051
M0162	0.2824	23.7718	159.54	17.5691	360.68	13.7528	102.67	0.0855
M0162A	0.2741	23.1639	173.19	20.545	315.45	16.0423	82.891	0.1118
M0163	0.3136	25.5557	167.88	21.327	295.52	15.2653	88.1606	0.1405
M0165	0.353	26.479	146.28	21.6739	383.93	16.7001	134.71	0.1161
M0166	0.3115	23.1835	135.16	13.3274	178.79	11.9103	52.0216	0.09636
M0167	0.2133	23.7222	130.36	14.575	305.14	16.3598	61.2503	0.1117
M0168	0.2528	24.7619	164.38	22.8153	366.44	14.4128	94.6361	0.0767
M0169	0.2894	27.0406	148.28	25.951	410.3	15.8246	116.71	0.09872
M0173	0.4405	24.4726	123.04	14.2713	71.2676	13.8858	29.2501	0.07875
M0174	0.2909	25.1809	180.29	24.8375	331.95	13.6561	94.1663	0.09403
M0176	0.292	23.9799	137.02	17.2898	320.46	15.294	94.2035	0.08712
M0177	0.2657	25.4704	176.04	23.0073	349.43	15.077	101.88	0.09434
M0178	0.2492	25.2263	137.95	18.3988	396.13	16.0093	97.3767	0.09635
M0179	0.2902	24.0576	170.56	16.8995	327.82	11.9587	94.6252	0.092
M0180	0.2919	22.8705	162.28	16.442	374.74	13.5485	108.21	0.1347
M0181	0.311	24.5617	163.63	20.7001	256.84	14.876	80.6009	0.0804
M0185	0.2911	24.0986	141.05	17.0724	317.47	14.5066	91.5705	0.1214
M0187	0.2653	27.1713	128.56	17.6086	334.19	15.808	84.7787	0.0639
M0188	0.2841	27.8481	163.77	23.3796	303.07	14.8145	86.8909	0.1142
M0189	0.2773	25.3578	152.47	25.9437	423.74	16.3155	130.98	0.07599
M0191	0.3113	23.7849	133.85	16.2401	251.39	12.544	77.3162	0.1054
M0192	0.1874	28.6134	148.54	19.1835	305.84	19.6274	65.5879	0.0724
M0194	0.2666	27.0868	161.53	20.5639	270.29	16.8239	79.1942	0.08731
M0195	0.2366	25.2539	116.37	16.1128	46.4946	NA	13.6894	0.0936
M0196	0.291	25.3522	140.1	13.0056	128.08	14.6225	32.4887	0.1167

Figure 6J

Genotype	lsmean_akw	lsmean_cd	lsmean_cl	lsmean_cw	lsmean_kc	lsmean_krn	lsmean_kw	lsmean_sdw
M0197	0.2796	25.8741	137.86	20.9658	246.14	15.6678	67.1649	0.08431
M0198	0.3059	24.2436	177.27	22.0155	423.88	13.3227	130.08	0.09647
M0199	0.1695	18.596	107.12	7.0855	118.15	12.0171	29.6543	0.1065
M0200	0.2613	25.316	188.94	26.2854	415.29	14.0445	103.7	0.09531
M0201	0.2761	21.596	149.72	17.824	357.73	19.6372	111.92	0.1141
M0203	0.2956	25.8442	170.02	23.088	305.36	15.4349	89.6992	0.1084
M0204	0.2429	22.7629	132.92	14.9541	332.76	13.105	84.5998	0.1118
M0205	0.2452	27.0949	184.74	26.1236	493.62	16.0734	118.1	0.09942
M0206	0.2907	23.4411	163.68	17.5708	194.02	13.4001	54.393	0.1442
M0208	0.3218	23.5785	129.17	14.9614	208.28	16.3418	62.3054	0.07286
M0209	0.2823	23.6946	137.6	16.2824	216.93	14.2696	61.3386	0.09693
M0210	0.2527	22.7121	185.74	19.7967	324.14	11.9709	79.7276	0.1344
M0212	0.2914	23.6281	179.39	19.0141	378.81	12.5711	113.24	0.07946
M0213	0.306	24.9787	159.31	21.1388	313.9	13.0931	96.6459	0.08223
M0214	0.1958	22.5043	163.49	16.506	369.61	15.1405	73.9868	0.09511
M0215	0.3184	26.5356	182.38	31.2732	419.18	14.3057	132.71	0.09726
M0216	0.2807	24.0593	153.22	17.8502	343.01	12.4833	95.7728	0.1173
M0217	0.2214	25.9141	136.37	18.1588	364.88	15.7945	76.6421	0.07422
M0218	0.2549	22.8324	123.44	10.0161	226.22	14.3533	55.9293	0.09818
M0219	0.2867	23.073	163.88	15.7817	280.13	13.7511	79.4692	0.1074
M0220	0.2687	25.7242	150.15	21.6532	379.39	17.8043	100.58	0.118
M0222	0.2906	24.6608	137.38	14.8736	370.83	15.4975	106.3	0.09854
M0223	0.2999	24.7085	145.35	24.1285	334.38	15.3013	106.41	0.08922
M0225	0.2185	24.2067	130.1	15.3847	91.3228	14.1201	20.8435	0.1178
M0228	0.2902	21.6925	122.99	11.1139	163.15	14.9936	44.3065	0.1037
M0229	0.2451	25.1746	154.08	18.518	407.31	16.1138	98.8235	0.0844
M0230	0.3046	25.3017	172.92	20.3339	277.55	11.0514	81.2427	0.09568
M0232	0.3434	23.7381	151.18	16.8803	291.07	14.3209	100.57	0.1227
M0233	0.2041	24.935	134.74	19.5714	402.38	16.266	81.7721	0.08616
M0234	0.2651	24.322	147.17	15.5038	340.03	15.5862	89.6195	0.07116
M0235	0.2489	22.2236	160.42	18.8799	341.04	14.7294	84.7369	0.1107
M0236	0.2864	24.004	147.09	18.4507	317.24	12.9094	90.5313	0.06173
M0238	0.1827	19.4856	137.9	12.7126	33.3034	15.8872	11.3099	0.09811
M0239	0.2529	29.0872	150.33	22.1421	464.59	16.3794	108.5	NA
M0240	0.1866	24.1024	134.25	15.4556	486.94	15.5183	90.311	0.068
M0241	0.2842	21.4682	119.44	18.0323	336.16	14.733	95.072	0.1116
M0244	0.2478	23.135	113.51	11.5728	221.43	13.3861	53.8798	NA
M0245	0.2692	29.8548	182.37	33.0054	452.54	14.7033	121.13	0.0883
M0248	0.2554	21.334	162.26	14.6516	174.71	13.5687	54.9607	0.09039
M0249	0.2919	24.3405	145.54	19.1235	323.42	14.8754	86.199	0.1339
M0251	0.276	22.9278	116.18	12.7908	201.06	14.4239	50.179	0.09623
M0252	0.2449	26.7228	152.17	20.6855	360.89	15.9236	91.3011	0.09373
M0254	0.2304	24.011	149.1	17.0301	401.72	14.5892	82.1079	0.1149
M0256	0.3086	29.5521	151.37	24.894	269.09	16.9634	77.1051	0.1009

Figure 6K

Genotype	lsmean_ akw	lsmean_ cd	lsmean_ cl	lsmean_ cw	lsmean_ kc	lsmean_ krn	lsmean_ kw	lsmean_ sdw
M0257	0.2999	24.1846	170.37	17.1247	359.34	13.8396	109.45	0.07295
M0258	0.1866	21.1554	146.52	18.1995	500.13	16.6051	96.127	0.1102
M0259	0.3563	26.2594	155.51	22.8052	344.77	15.0984	121.2	0.08977
M0260	0.2976	25.2391	160.1	20.5632	308.89	12.358	91.4414	0.06664
M0262	0.28	23.3619	133.93	14.2789	229.79	13.4658	62.3412	0.1131
M0263	0.2423	24.1342	139.09	16.9829	382.41	17.4087	81.2054	0.09423
M0264	0.2215	25.7326	146.36	20.1822	419.44	15.855	93.5209	0.08673
M0265	0.2673	24.9552	122.65	16.4177	331.47	15.4946	87.1081	0.07195
M0266	0.244	25.699	152.52	21.6261	482.04	16.9069	117.78	0.1162
M0267	0.2334	25.3185	158.34	20.6625	424.93	16.2458	98.4339	0.1119
M0269	0.2262	22.6754	128.97	11.7433	169.56	13.4445	36.7842	0.0792
M0270	0.2415	26.6402	179.84	27.9354	123.61	14.0928	45.4136	0.07657
M0271	0.3039	23.6061	147.13	15.9189	298.72	14.2944	92.7942	0.09701
M0272	0.2607	23.0575	146.55	17.8069	326.2	17.0172	82.5903	0.09348
M0273	0.2724	28.319	139.81	28.3417	445.59	16.5044	120.12	0.08418
M0274	0.2223	24.3487	156.72	17.2633	460.25	15.9013	104.32	0.0726
M0275	0.2607	30.7555	154.12	21.912	422.68	19.7781	104.83	0.08412
M0276	0.2911	23.0438	176.83	19.8375	378.6	14.1165	109.14	0.1083
M0279	0.2417	22.2687	110.1	9.4424	19.4112	12.3061	3.7686	0.09919
M0280	0.2795	23.8347	164.39	18.251	349.37	12.983	95.5819	0.1001
M0281	0.2751	22.753	133.04	7.3662	29.8277	NA	10.9731	0.05963
M0282	0.2954	21.7818	134.37	16.2371	158.55	13.2619	46.6278	0.1161
M0283	0.1828	18.9353	109.98	8.3272	0.5002	NA	2.5462	0.09509
M0284	0.246	27.2197	181.48	21.5533	452.76	16.6071	104.7	0.1054
M0285	0.2798	23.0453	191.64	21.419	283.23	12.2523	84.4461	0.08449
M0286	0.2445	21.9973	135.04	13.5616	37.5775	12.8111	9.6769	0.1158
M0287	0.3297	25.47	136.84	22.6845	295.87	15.5608	88.223	0.08502
M0288	0.3349	25.445	143.13	19.1967	393.11	16.4407	130.82	0.09806
M0289	0.2583	21.864	146.81	15.1897	366.86	12.6921	93.6425	0.0759
M0290	0.2908	24.1468	148.51	18.2635	337.09	14.5896	96.4849	0.1101
M0291	0.2655	24.8609	172.08	20.9066	438.29	15.2894	114.91	0.08267
M0292	0.3396	22.3407	149.56	14.6731	225.42	10.5492	78.5753	0.1011
M0293	0.3267	25.6775	146.92	20.5833	354.77	13.3144	116.01	0.1117
M0294	0.2229	20.7723	115.8	12.8441	305.68	14.4636	70.6006	0.08844
M0295	0.2442	22.7898	151.19	15.6862	364.97	13.4814	85.424	0.09211
M0296	0.2958	25.2823	154.71	21.0685	262.85	13.1573	75.9461	0.06002
M0297	0.2728	25.4376	146.77	19.9809	416.55	16.1897	113.08	0.1213
M0298	0.2201	25.6057	148.09	17.1711	418.62	16.5921	89.9993	0.1069
M0300	0.3349	24.4955	129.32	21.7224	255.19	14.0276	85.7386	0.07172
M0303	0.2716	23.3641	145.01	15.3916	247.49	13.6487	73.5629	0.09915
M0304	0.2711	21.6892	105.17	17.2965	188.73	12.0782	53.108	0.08716
M0305	0.1539	19.7708	132.8	8.9658	120.5	13.0736	21.7325	0.05864
M0306	0.247	NA	NA	15.7372	286.49	14.0441	71.8338	0.1064
M0307	0.2318	26.297	152.05	21.9639	304.04	15.294	66.4026	0.06978

Figure 6L

Genotype	lsmean_ akw	lsmean_ cd	lsmean_ cl	lsmean_ cw	lsmean_ kc	lsmean_ krn	lsmean_ kw	lsmean_ sdw
M0308	0.2148	18.0556	98.3949	4.0783	-3.2975	NA	-2.1399	0.08526
M0309	0.336	23.8272	155.51	19.8353	317.58	15.2499	103.93	0.09775
M0310	0.2033	24.7179	145.11	18.6061	388.39	15.948	80.1751	0.07343
M0311	0.2527	21.9354	116.89	11.8732	322.32	14.7487	80.5793	0.0909
M0312	0.2514	24.5045	178.5	30.3517	446.71	13.9341	111.51	0.1287
M0313	0.3161	23.5864	134.3	16.9848	301.22	12.2671	95.5243	0.09755
M0317	0.2713	23.4783	173.91	19.1884	379.63	12.3361	101.24	0.09572
M0318	0.2233	22.941	153.43	15.748	344.55	14.4618	72.5104	0.09028
M0320	0.2645	25.4018	173.43	23.4696	422.93	14.4893	110.51	0.09993
M0321	0.3049	25.4205	152.58	20.0155	428.4	16.7179	129.33	0.1137
M0322	0.2397	22.5943	115.75	14.3837	279.21	15.1023	64.0657	0.06259
M0323	0.2573	23.4904	165.54	17.0118	379.32	13.4905	97.8744	0.1034
M0324	0.3378	23.729	137.31	14.7897	146.97	13.633	49.5278	0.08131
M0325	0.2513	24.3216	175.01	22.1197	404.39	15.2	106.63	0.09303
M0326	0.1215	21.0013	129.23	12.2605	204.7	13.7591	33.541	0.1023
M0327	0.2771	22.8367	179.48	17.1804	366.12	14.5507	102.42	0.1122
M0328	0.2956	24.6435	147.45	19.5209	316.44	13.8742	93.456	0.09241
M0331	0.2929	24.2381	143.08	16.7121	293.41	14.6447	81.5889	0.1039
M0334	0.2231	24.8902	144.62	16.5623	366.16	15.1734	78.4779	0.09752
M0335	0.2946	22.7087	156.31	17.075	312.34	12.6934	91.311	0.108
M0337	0.2677	23.6878	134.48	22.174	228.6	12.3852	76.5458	0.1089
M0338	0.2468	25.4218	182.96	26.2111	447.01	13.9813	109.64	0.1277
M0339	0.2306	24.9967	119.47	14.8356	417.92	17.1087	96.3156	0.1056
M0341	0.2095	25.2423	134.7	17.2159	246.13	14.3852	63.7765	0.0946
M0342	0.2872	21.0225	117.71	12.1551	197.33	13.3427	55.6466	0.0865
M0344	0.2833	22.8881	169.36	16.7086	185.76	12.4144	55.9101	0.07709
M0345	0.3281	23.3266	176.84	18.5327	242.13	12.651	81.166	0.1058
M0348	0.3028	23.4779	151.55	17.9803	255.41	12.0374	69.4963	0.07294
M0350	0.3151	20.747	150.72	11.5342	126.07	11.6767	39.0418	0.1128
M0351	0.2721	22.2649	116.47	11.6929	186.38	12.8964	54.5875	0.08234
M0352	0.2209	24.9655	170.84	18.8996	451.94	16.6239	102.53	0.1062
M0353	0.2472	23.5305	167.47	18.9834	427.11	16.0773	105.08	0.06816
M0354	0.2534	20.8977	125.89	13.7156	263.13	14.1823	68.2192	0.0964
M0355	0.2648	21.331	130.23	9.4724	117.19	12.3511	30.8181	0.09217
M0357	0.2072	23.5229	140.98	12.5535	294.61	13.6932	61.2388	0.08476
M0358	0.2416	25.6616	160.84	22.9718	363.8	15.9111	80.15	0.06746
M0360	0.2663	20.1478	168.61	19.1287	273.3	11.9379	68.7346	0.07339
M0362	0.3369	22.9738	107.89	12.7632	123.9	14.0382	49.0688	0.07848
M0364	0.2373	23.0419	126.64	13.4366	292.42	15.1136	68.0475	0.1186
M0365	0.2302	25.4783	116.4	16.4065	242.19	16.8469	69.2058	0.1116
M0366	0.2445	22.963	151.16	15.3707	255.77	12.4324	60.2635	0.11
M0368	0.2954	27.5083	176.59	26.7901	412.2	13.8774	120.2	0.108
M0369	0.257	23.6922	178.92	19.8305	414.55	14.3088	105.02	0.1009
M0370	0.3107	25.1501	122.61	19.4652	316.89	16.1093	100.02	0.1381

Figure 6M

Genotype	lsmean_akw	lsmean_cd	lsmean_cl	lsmean_cw	lsmean_kc	lsmean_krn	lsmean_kw	lsmean_sdw
M0375	0.2471	23.4912	130.3	13.049	216.51	13.2534	54.389	0.08939
M0376	0.2503	21.6615	175.62	18.8457	368.66	12.2868	106.93	0.08762
M0377	0.2186	25.2985	126.09	14.5483	320.82	15.2463	67.0258	0.08628
M0378	0.2396	20.8781	137.05	11.5684	257.17	13.8212	63.7104	0.1103
M0379	0.2393	22.5358	168.45	13.5531	204.11	12.0108	45.5712	0.09987
M0380	0.2577	22.4476	142.49	15.0271	180.48	12.2394	48.7967	0.1023
M0381	0.3089	22.9861	126.77	12.883	257.87	12.5015	79.5759	0.1336
M0382	0.2581	23.352	161.71	18.4483	365.83	14.7327	92.6613	0.08547
M0383	0.282	24.8245	135.05	22.6208	267.83	13.2136	74.1625	0.08242
M0384	0.2434	21.1185	150.64	12.6687	77.7311	12.1523	27.1647	0.1165
Mo17	0.326	21.3603	176.58	16.1485	221.03	10.8271	75.1197	0.101
Mo17xB73	0.3717	27.3749	221.64	39.126	733.22	15.5605	273.35	0.1494
Mo17xM0001	0.3292	25.589	199	32.7715	519.97	13.5329	172.96	0.124
Mo17xM0002	0.3343	24.2291	213.17	29.2144	579.9	13.6167	195.26	0.1263
Mo17xM0004	0.3369	23.1065	185.82	20.6828	444.37	11.5294	150.73	0.1097
Mo17xM0005	0.3288	23.6078	198.31	21.4266	515.37	12.1683	179.02	0.1347
Mo17xM0006	0.3118	22.9798	204.33	19.91	483.94	11.7846	152.31	0.1296
Mo17xM0007	0.3923	25.9142	214.16	27.8323	448.03	12.1219	175.86	0.108
Mo17xM0008	0.3672	25.732	218.74	27.7176	581.4	13.0197	213.07	0.1158
Mo17xM0010	0.3108	22.6415	193.66	18.3836	503.88	13.7138	154.14	0.1094
Mo17xM0011	0.3576	25.2476	209.69	35.1643	519.93	12.1703	184.78	0.1246
Mo17xM0012	0.3473	25.74	226.03	29.8849	587.2	13.5967	200.69	0.145
Mo17xM0013	0.3061	24.3326	204.21	25.9327	583.8	13.4829	178.87	0.1237
Mo17xM0014	0.3304	23.3643	178.57	22.8779	406.62	12.7537	128.66	0.1051
Mo17xM0015	0.3696	24.6068	205.54	26.9565	539	12.8157	197.71	0.1223
Mo17xM0016	0.3412	25.2775	217.76	34.8172	574.72	12.3185	196.42	0.1365
Mo17xM0017	0.3311	23.6853	208.88	29.5142	525.57	12.8115	174.38	0.1159
Mo17xM0021	0.3212	24.0545	191.36	23.1916	528.93	13.0968	171.96	0.1435
Mo17xM0022	0.3632	25.5703	185.19	26.5524	416.01	13.4936	159.91	0.1323
Mo17xM0023	0.3483	23.7251	212.7	23.4047	496.82	12.5753	170.22	0.1132
Mo17xM0024	0.3168	22.1523	184.82	18.5635	347.74	11.1383	104.14	0.131
Mo17xM0025	0.3406	26.3005	210.13	32.8748	594.03	13.6484	202.73	0.143
Mo17xM0026	0.3606	25.5119	201.67	31.068	491.98	13.0436	176.53	0.127
Mo17xM0027	0.3668	23.8429	211.26	24.4733	472.84	11.7812	175.03	0.1447
Mo17xM0028	0.3122	22.1078	186.21	21.5075	449.72	12.5868	144.8	0.1256
Mo17xM0029	0.3621	24.4093	212.2	25.4608	543.55	13.21	196.08	0.1172
Mo17xM0030	0.3172	24.044	189.07	28.8641	424.81	13.6589	153.17	0.1395
Mo17xM0031	0.3755	24.7297	210.79	28.1814	539.62	13.3295	202.79	0.1222
Mo17xM0032	0.3766	24.4955	214.09	26.9437	457.1	12.0422	170.9	0.1068
Mo17xM0033	0.3623	24.4479	211.2	25.2707	517.79	12.3109	184.8	0.1279
Mo17xM0034	0.3373	27.3267	212.64	32.8029	714.93	15.6426	240.91	0.1427
Mo17xM0035	0.3613	24.2225	227.57	26.1711	562.15	11.9854	201.61	0.1301
Mo17xM0039	0.3857	25.9037	204.6	29.632	495.67	12.503	193.37	0.1125
Mo17xM0043	0.3575	25.0735	206.35	28.0295	578.71	13.9351	204.83	0.2042

Figure 6N

Genotype	lsmean_ akw	lsmean_ cd	lsmean_ cl	lsmean_ cw	lsmean_ kc	lsmean_ krn	lsmean_ kw	lsmean_ sdw
Mo17xM0044	0.3112	24.0249	196.42	22.2211	473.24	12.5285	150.9	0.08299
Mo17xM0045	0.3475	24.6216	209.83	24.2972	576.46	13.1947	199.34	0.09709
Mo17xM0046	0.2982	20.769	175.13	20.3448	298.51	12.4337	90.8952	0.08974
Mo17xM0047	0.3538	23.3071	203.88	19.8693	524.29	13.0451	185.93	0.1267
Mo17xM0048	0.3472	22.7637	178.25	21.2321	352.04	12.1082	122.93	0.1209
Mo17xM0051	0.3719	23.4592	205.5	26.2278	501.55	13.8278	186.03	0.1336
Mo17xM0052	0.3341	21.8504	166.77	18.5544	332.24	12.5264	116.54	0.1483
Mo17xM0053	0.3142	22.818	160.68	18.3705	339.75	13.1865	113.24	0.1251
Mo17xM0054	0.3544	25.447	206.79	22.9819	540.94	13.9056	193.69	0.1554
Mo17xM0055	0.3634	26.1258	202.25	28.7379	592.02	12.9075	214.6	0.1192
Mo17xM0056	0.3186	24.3639	210.47	29.3755	614.21	14.2249	197.72	0.1178
Mo17xM0057	0.3497	25.9589	228.08	28.6389	518.03	12.9247	193.68	0.1204
Mo17xM0058	0.331	26.4322	210	31.2761	623.97	14.9586	204.12	0.1255
Mo17xM0059	0.3415	25.0164	182.83	26.1268	474.54	13.0205	174	0.1386
Mo17xM0060	0.3574	25.4476	197.51	31.5136	462.82	13.0901	172.11	0.1489
Mo17xM0061	0.3756	25.1141	219.38	32.3235	579	12.3185	218.02	0.1302
Mo17xM0064	0.3652	24.4338	203.87	28.5139	483.3	13.0335	180.5	0.1322
Mo17xM0065	0.3133	23.1754	173.42	20.89	449.62	14.3665	154.95	0.1554
Mo17xM0066	0.3292	25.91	200.72	27.4343	587.06	14.5587	195.82	0.1344
Mo17xM0067	0.3635	24.2395	212.89	26.2109	477.99	12.0348	172.84	0.08265
Mo17xM0069	0.306	24.5269	212.5	29.0517	542.61	13.7911	161.3	0.1677
Mo17xM0070	0.3206	22.7369	192.53	19.7383	474.11	12.5235	150.56	0.1192
Mo17xM0071	0.3439	23.1505	186.22	22.6144	485.93	13.4434	169.57	0.1347
Mo17xM0075	0.3406	24.1307	213.05	29.6919	521.6	12.5851	178.06	0.1254
Mo17xM0076	0.351	24.9538	205.13	28.4091	495.38	14.4214	178.41	0.1421
Mo17xM0077	0.3579	23.6924	217.94	25.1234	528.46	12.3159	187.34	0.1298
Mo17xM0078	0.3675	25.7433	213.85	34.3091	581.98	13.963	214.97	0.1388
Mo17xM0079	0.3522	23.0973	186.36	22.2283	390.63	12.2572	141.62	0.09293
Mo17xM0080	0.331	24.3271	192.57	28.1078	541.2	13.2271	180.47	0.1294
Mo17xM0081	0.3314	24.0764	196.17	27.1971	513.21	12.5526	168.81	0.1336
Mo17xM0083	0.3345	25.3749	193.44	26.0137	526.07	12.2935	176.49	0.1435
Mo17xM0084	0.3594	23.1825	183.2	20.5753	423.51	11.8219	151.94	0.1081
Mo17xM0085	0.3441	23.8008	208.77	28.9787	568.85	13.5612	193.57	0.1477
Mo17xM0086	0.2762	20.4987	148.52	15.7812	352.07	12.8711	108.72	0.1374
Mo17xM0088	0.388	24.9941	188.75	28.0482	344.74	12.2684	127.64	0.1294
Mo17xM0090	0.3385	22.912	196.9	21.6951	465.88	12.6685	164.01	0.1416
Mo17xM0091	0.3459	23.8121	193.93	22.669	486.93	12.8497	173.13	0.1321
Mo17xM0092	0.3409	23.0974	181.05	17.1792	437.09	11.9936	147.93	0.1383
Mo17xM0093	0.3576	23.114	214.55	24.395	425.63	12.636	153.64	0.1303
Mo17xM0095	0.3207	24.8166	218.33	26.9185	623.86	13.8804	199.83	NA
Mo17xM0096	0.2985	20.0712	149.11	15.8652	370.02	13.8433	120.36	0.1198
Mo17xM0097	0.343	24.47	211.17	27.1119	625.65	14.0363	213.81	0.1133
Mo17xM0098	0.3265	24.0971	208.06	24.1624	562.96	13.3876	183.53	0.1173
Mo17xM0099	0.3455	24.0314	199.25	26.4859	392.6	12.5319	135.01	0.1457

Figure 6O

Genotype	lsmean_ akw	lsmean_ cd	lsmean_ cl	lsmean_ cw	lsmean_ kc	lsmean_ krn	lsmean_ kw	lsmean_ sdw
Mo17xM0100	0.3196	22.6019	178.1	19.9671	394.68	11.4085	127.81	0.1192
Mo17xM0101	0.3652	24.1397	200.39	22.9826	529.5	13.0352	194.59	0.113
Mo17xM0102	0.2968	24.6207	214.47	27.0091	653.63	14.4635	193.32	0.143
Mo17xM0103	0.3467	23.6136	209.49	25.0628	474.86	12.8985	175.47	0.1407
Mo17xM0104	0.3806	23.9378	207.58	25.2913	531.26	12.2903	200.94	0.1057
Mo17xM0105	0.3593	24.4321	177.9	27.129	455.52	13.1482	166.72	0.1043
Mo17xM0106	0.3569	22.5023	187.9	20.0262	439.2	11.9459	158.47	0.1372
Mo17xM0107	0.3161	25.0951	216.94	29.7193	628.64	13.8215	198.56	0.1332
Mo17xM0109	0.3178	21.9753	197.2	20.1503	470.73	12.3856	161.81	0.1247
Mo17xM0110	0.3516	24.5437	190.14	26.9694	397.87	12.6189	140.79	0.1198
Mo17xM0113	0.3421	25.5772	184.72	25.3269	577.56	14.626	198.22	0.1221
Mo17xM0114	0.3398	25.2711	242.26	31.4305	709.02	14.6744	241.23	0.1219
Mo17xM0115	0.333	24.947	223.74	24.2984	526.83	12.2273	174.91	0.1312
Mo17xM0116	0.3751	22.5513	187.22	20.1254	388.99	11.4322	153.85	0.1285
Mo17xM0117	0.3382	24.0146	215.5	27.7405	490.3	13.2666	165.31	0.0981
Mo17xM0118	0.3296	24.3752	191.92	27.0487	505.57	13.6816	177.41	0.09582
Mo17xM0120	0.3402	23.6661	189.06	23.0984	488.42	13.3757	167.07	0.1272
Mo17xM0121	0.3585	25.1087	217.6	29.5899	572.52	13.4964	201.16	0.1379
Mo17xM0122	0.3605	23.9661	180.08	24.0079	437.15	13.4262	159.53	0.1406
Mo17xM0123	0.3383	22.7834	193.67	21.0316	402.25	12.5635	142.09	0.1059
Mo17xM0124	0.3628	24.0603	187.2	23.7019	439.79	13.2077	161.49	0.1115
Mo17xM0125	0.3349	25.8483	222.44	34.7503	645.24	14.6928	208.64	0.1203
Mo17xM0126	0.3591	23.3696	214.38	23.8099	519.21	12.116	185.28	0.1145
Mo17xM0127	0.3391	24.1681	210.11	26.2231	499.69	13.0002	171.32	0.1002
Mo17xM0129	0.3618	25.5502	222.71	28.0793	457.34	12.5851	164.36	0.1296
Mo17xM0130	0.3208	23.3755	206.68	23.7616	566.85	14.1638	182.02	0.1649
Mo17xM0131	0.3446	23.3595	200.01	19.6122	464.37	12.2311	159	0.1134
Mo17xM0132	0.3372	24.2619	179.69	21.3052	440.73	12.4775	152.16	0.1451
Mo17xM0133	0.3163	24.3286	192.71	27.5149	487.09	13.0308	159.65	0.1404
Mo17xM0138	0.3587	23.8927	194.47	24.1852	476.71	12.6324	171.19	0.1272
Mo17xM0141	0.3655	25.1098	188.74	24.518	511.39	13.2403	185.56	0.1028
Mo17xM0142	0.3108	24.1896	206.58	23.3243	612.53	13.9869	189.41	0.1209
Mo17xM0143	0.3495	25.2318	202.32	28.6721	499.8	13.6148	173.25	0.1444
Mo17xM0144	0.3251	24.9116	203.99	29.2227	584.13	13.5414	189.13	0.1455
Mo17xM0145	0.3479	25.7757	187.7	25.615	478.89	13.6354	168.65	0.1553
Mo17xM0147	0.3127	23.084	192.5	21.9672	466.78	12.9292	152.9	0.1207
Mo17xM0149	0.3153	24.9901	209.26	26.1957	552.37	14.1954	171.29	0.1081
Mo17xM0150	0.3554	22.8447	215.13	21.7425	458.91	11.8625	162.87	0.08831
Mo17xM0151	0.3344	24.4134	191.15	21.3736	465.72	12.2654	152.3	0.1082
Mo17xM0152	0.3877	24.8362	204.58	26.251	375.05	12.7945	146.15	0.1109
Mo17xM0154	0.3355	23.6465	207.35	24.7405	486.1	12.7343	165.45	0.1137
Mo17xM0155	0.3597	23.463	202.04	23.5254	505.79	12.2849	182.39	0.1239
Mo17xM0156	0.3577	25.1249	192.48	25.3355	529.1	13.7207	186.61	0.1394
Mo17xM0157	0.3484	24.3933	207.39	24.1341	556.94	13.7473	194.18	0.1368

Figure 6P

Genotype	lsmean_akw	lsmean_cd	lsmean_cl	lsmean_cw	lsmean_kc	lsmean_krn	lsmean_kw	lsmean_sdw
Mo17xM0160	0.3586	25.4465	216.87	27.0609	595.33	13.72	214.11	0.1288
Mo17xM0160A	0.3573	25.3038	195.66	31.4181	540.04	14.5503	210.31	0.1185
Mo17xM0161	0.3496	23.3755	215.1	27.4266	493.91	12.8375	175.86	0.1318
Mo17xM0162	0.3557	24.6492	190.27	22.4739	446.98	13.1806	156.38	0.1198
Mo17xM0162A	0.3299	25.0361	218.27	29.4889	607.56	15.4187	200.75	0.1329
Mo17xM0163	0.3507	24.481	213.58	27.5261	545.43	13.0577	191.61	0.1142
Mo17xM0165	0.3535	25.5016	194.75	27.7416	634.11	14.4773	221	0.112
Mo17xM0166	0.3528	24.021	194.73	24.0391	478.95	12.7931	168.71	0.1214
Mo17xM0167	0.3071	23.3873	178.18	21.5124	483.06	13.6352	148.38	0.1048
Mo17xM0168	0.358	24.6389	215.2	30.1138	519.3	12.3972	186.36	0.1194
Mo17xM0169	0.3402	24.2545	190.99	25.939	494.19	12.5193	175.05	0.1132
Mo17xM0173	0.3413	24.4096	193.93	30.8415	559.61	14.4075	217.82	0.1101
Mo17xM0174	0.365	24.5771	216.9	28.4842	520.09	12.0197	190.58	0.1307
Mo17xM0176	0.3953	23.8671	213.01	28.5486	560.55	13.4395	225.1	0.144
Mo17xM0177	0.3909	24.7124	209.84	27.7181	486.58	13.0288	192.77	0.1313
Mo17xM0178	0.3183	24.445	196.48	26.1697	596.26	14.129	189.46	0.1358
Mo17xM0179	0.356	24.6701	216.84	27.3977	541.72	11.962	193.21	0.1578
Mo17xM0180	0.3563	23.6754	207.94	22.2613	542.19	12.2639	191.96	0.1446
Mo17xM0181	0.3613	25.5033	218.87	27.6201	470.22	13.0819	172.52	0.1235
Mo17xM0185	0.2323	23.5898	155.62	19.1004	349.45	15.1689	125.28	0.1352
Mo17xM0187	0.334	24.961	179.27	22.9248	488.9	13.457	169.48	0.1354
Mo17xM0188	0.3641	25.9041	214.4	30.9386	603.57	13.7244	219.04	0.1264
Mo17xM0189	0.3536	24.7291	216.74	29.2261	594.39	13.6478	210.83	0.1201
Mo17xM0191	0.3324	23.9394	181.83	23.0021	456.41	13.0866	151.74	0.1127
Mo17xM0192	0.3074	25	181.41	21.043	451.21	15.1135	153.79	0.1366
Mo17xM0194	0.3617	25.107	192.26	26.1453	411.25	14.1657	148.93	0.1205
Mo17xM0195	0.3411	24.1048	190.43	25.9727	383.81	12.0036	136.73	0.1324
Mo17xM0196	0.3089	24.6279	202.83	27.7867	540.84	13.5482	174.85	0.1395
Mo17xM0197	0.3509	25.478	203.19	29.7462	548.29	14.1887	191.79	0.1177
Mo17xM0198	0.3675	24.1063	219.72	26.885	556.74	12.9745	205.67	0.1457
Mo17xM0199	0.3102	21.7314	203.42	21.5263	524.95	12.0598	163.37	0.1507
Mo17xM0200	0.3524	24.942	216.89	27.0349	519.37	12.8094	183.95	0.141
Mo17xM0201	0.3401	25.488	222.42	28.5652	689.12	14.414	236.07	0.1298
Mo17xM0203	0.34	25.2699	201.09	26.6001	554.19	14.1766	192.29	0.1275
Mo17xM0204	0.3348	23.8233	193.06	25.3176	581.37	13.0381	195.1	0.139
Mo17xM0205	0.3286	25.3252	207.41	26.8855	580.67	14.0323	195.17	0.1224
Mo17xM0206	0.3056	22.5379	185.87	21.1658	454.3	13.0276	145.49	0.1388
Mo17xM0208	0.3396	23.8516	190.92	25.1743	473.64	13.2513	159.9	0.1346
Mo17xM0209	0.3502	25.856	211.01	29.4304	500.47	13.973	178.58	0.1161
Mo17xM0210	0.3126	23.7585	219.45	24.5247	518.44	12.1195	161.47	0.1406
Mo17xM0212	0.3735	24.2657	208.53	24.6627	476.96	11.6382	179.19	0.09949
Mo17xM0213	0.3534	24.4513	213.27	28.3455	533.13	12.9171	187.58	0.1191
Mo17xM0214	0.3434	22.0892	194.1	23.8169	496.01	13.8695	171.35	0.1098
Mo17xM0215	0.3499	24.9518	187.82	26.5696	438.77	12.7085	153.71	0.1146

Figure 6Q

Genotype	lsmean_akw	lsmean_cd	lsmean_cl	lsmean_cw	lsmean_kc	lsmean_krn	lsmean_kw	lsmean_sdw
Mo17xM0216	0.3698	23.8989	199.79	24.7593	485.09	12.8699	182.52	0.1287
Mo17xM0217	0.3106	26.1435	203.79	27.6627	602.63	14.2027	185.73	0.1307
Mo17xM0218	0.3361	24.0773	194.57	22.3426	548.71	13.4969	183.65	0.1295
Mo17xM0219	0.3407	23.9112	207.31	22.5634	522.77	12.9064	179.04	0.1326
Mo17xM0220	0.3399	25.8341	213.95	31.838	670.77	15.1168	227.14	0.1182
Mo17xM0222	0.3519	24.4208	193.48	23.3425	534.57	13.4081	187.68	0.136
Mo17xM0223	0.3576	23.6806	171.51	25.8985	477.27	12.9272	176.36	0.1256
Mo17xM0225	0.3391	24.8512	205.15	27.9149	510.02	13.2007	173.82	0.1272
Mo17xM0228	0.3225	24.0363	202.51	23.8185	600.72	14.1954	191.71	0.1232
Mo17xM0229	0.3102	23.4172	173.89	21.1197	442.42	13.0299	150.79	0.1276
Mo17xM0230	0.37	25.0676	214.55	26.7255	470.09	12.1924	174.54	0.129
Mo17xM0232	0.3497	24.6405	205.47	24.3964	522.1	13.6058	180.47	0.1015
Mo17xM0233	0.3351	25.3123	219.52	32.3151	639.5	13.6364	213.02	0.1373
Mo17xM0234	0.3382	24.9572	190.18	22.9249	494.79	13.7109	169.37	0.1161
Mo17xM0235	0.3523	23.8072	213.05	26.6166	545.65	13.6485	191.23	0.1204
Mo17xM0236	0.3436	25.3021	214.13	30.9313	605.79	12.7095	204.85	0.1423
Mo17xM0238	0.3158	23.2412	219.85	31.8936	639.52	14.7356	201.76	0.1406
Mo17xM0239	0.3178	25.4036	196.2	27.9979	578.84	14.302	202.47	NA
Mo17xM0240	0.3329	24.8775	208.26	29.1184	644.74	13.3038	213.18	0.1505
Mo17xM0241	0.3423	20.488	181.75	24.0237	461.87	12.9244	166.51	0.09144
Mo17xM0244	0.3514	25.0426	205.81	24.5584	537.75	12.936	188.67	NA
Mo17xM0245	0.3739	28.4757	230.48	38.3334	624.55	14.4262	234.83	0.1233
Mo17xM0248	0.3541	23.8465	224.32	25.4385	577.6	12.6952	203.84	0.1095
Mo17xM0249	0.2978	24.7566	158.82	21.2663	386.48	15.3511	110.85	0.1361
Mo17xM0251	0.3367	24.304	207.77	26.4176	503.63	12.76	169.06	0.1163
Mo17xM0252	0.345	26.0211	223.02	30.0027	621.19	13.7326	214.07	0.1348
Mo17xM0254	0.3324	24.7447	210.81	28.1119	593.63	13.2622	197.56	0.1479
Mo17xM0256	0.3322	27.8607	213.78	31.192	636.09	15.4099	210.97	0.1343
Mo17xM0257	0.3513	22.8228	187.96	22.0933	509.89	12.6595	179.2	0.1367
Mo17xM0258	0.3624	22.5338	206.65	26.0646	563.52	13.4076	204.1	0.1514
Mo17xM0259	0.3694	24.5732	195.5	24.1968	467.73	12.5013	175.78	0.1341
Mo17xM0260	0.3534	24.5113	193.19	23.4607	462.43	12.3603	161.99	0.119
Mo17xM0262	0.3395	23.9304	192.66	24.4279	449.69	13.5986	156.83	0.1441
Mo17xM0263	0.3325	24.8385	198.41	27.5668	588.03	13.6579	201.04	0.117
Mo17xM0264	0.3365	25.5482	193.37	24.9097	494.2	13.6317	164.02	0.1442
Mo17xM0265	0.3324	23.6188	172.28	23.3886	516.57	13.8985	171.04	0.1586
Mo17xM0266	0.3444	25.5833	195.6	26.6872	578.05	14.7822	200.56	0.1172
Mo17xM0267	0.3331	24.8103	211.21	27.7476	611.04	13.8332	204.91	0.1133
Mo17xM0269	0.3134	23.7898	192.37	24.0074	515.54	13.4181	162.75	0.106
Mo17xM0270	0.3592	25.4573	216.23	36.3001	530.37	13.1274	195.15	0.1324
Mo17xM0271	0.3544	22.9865	207.44	24.2569	505.34	13.3127	195.23	0.1567
Mo17xM0272	0.305	25.0142	206.89	30.0684	637.79	14.5514	196.03	0.1506
Mo17xM0273	0.3323	25.589	178.62	27.1193	525.34	14.2219	176.49	0.1274
Mo17xM0274	0.278	23.2078	196.98	21.2569	571.2	14.0684	169.94	0.1109

Figure 6R

Genotype	lsmean_ akw	lsmean_ cd	lsmean_ cl	lsmean_ cw	lsmean_ kc	lsmean_ krn	lsmean_ kw	lsmean_ sdw
Mo17xM0275	0.3471	28.2458	209.6	30.8284	748.44	16.2424	259.51	0.1184
Mo17xM0276	0.3412	24.0947	208.01	24.0693	557.62	13.6476	190.17	0.1234
Mo17xM0279	0.3653	23.8926	190.86	24.0718	456.67	13.7303	167.66	0.115
Mo17xM0280	0.3566	24.6674	210.84	24.1763	487.22	12.8492	175.66	0.1172
Mo17xM0281	0.4255	25.6704	219.92	32.0255	450.47	12.0555	189.44	0.1439
Mo17xM0282	0.3129	23.8223	192.61	25.9526	477.02	13.0503	157.46	0.1363
Mo17xM0283	0.3558	25.0516	209.98	29.4892	454.43	13.7783	163.03	0.1776
Mo17xM0284	0.3151	25.2282	210.39	24.7957	538.08	13.2369	170.62	0.1182
Mo17xM0285	0.3201	23.9798	229.11	26.2022	547.73	12.2808	173.35	0.1318
Mo17xM0286	0.3622	25.5915	205.92	32.8042	565.03	12.8913	207.47	0.1346
Mo17xM0287	0.3393	22.7063	177.24	23.3433	483.22	14.3107	176.29	0.1329
Mo17xM0288	0.3583	25.6958	197.39	25.5928	563.59	13.9471	202.18	0.1568
Mo17xM0289	0.3681	23.451	207.9	25.838	513.31	12.3036	189.44	0.1439
Mo17xM0290	0.3448	23.5917	178.3	19.7915	369.61	12.104	125.37	0.1267
Mo17xM0291	0.3315	24.3385	202.69	24.9778	548.79	14.4668	184.25	0.1246
Mo17xM0292	0.3593	23.4324	200.64	22.7367	471.81	11.8516	170.6	0.1204
Mo17xM0293	0.3536	23.4289	186.07	23.158	461.34	11.9839	169.62	0.1497
Mo17xM0294	0.3484	23.8402	197.31	27.6488	609.94	13.2119	212.69	0.1385
Mo17xM0295	0.3386	24.3694	220.85	28.7786	639.8	13.7065	217.49	0.1457
Mo17xM0296	0.3439	24.5072	187.26	23.6528	472.79	12.4487	161.85	0.1086
Mo17xM0297	0.3654	25.2707	197.22	27.5482	577.83	13.8716	210.29	0.1328
Mo17xM0298	0.3108	24.6457	193.86	24.2538	598.17	14.4051	186.61	0.1644
Mo17xM0300	0.3791	25.0186	212.4	31.6036	566.67	12.9787	213.9	0.1358
Mo17xM0303	0.3699	24.8288	215.1	29.5958	557.74	13.5309	204.45	0.107
Mo17xM0304	0.3797	23.4934	171.54	25.2406	389.98	12.4112	152.2	0.1368
Mo17xM0305	0.3676	22.5532	206.8	24.6156	266.47	13.162	98.6651	0.09489
Mo17xM0306	0.3641	24.7121	210.21	30.7755	585.47	13.0342	213.87	0.1044
Mo17xM0307	0.3591	25.6283	214.15	30.4453	532.59	13.5468	190.29	0.09582
Mo17xM0308	0.3806	24.9481	210.52	26.562	570.42	13.5002	214.18	0.1087
Mo17xM0309	0.3119	21.7152	167.35	19.7561	405.4	13.4675	142.17	0.1733
Mo17xM0310	0.3004	22.8893	176.03	20.6774	471.97	14.0245	146.44	0.1465
Mo17xM0311	0.344	23.1614	196.15	24.3297	539.19	13.7849	187.54	0.1376
Mo17xM0312	0.385	24.9864	211.36	34.6792	533.43	13.9398	203.5	0.1449
Mo17xM0313	0.3415	23.998	193.79	24.4978	475.17	12.071	160.47	0.1109
Mo17xM0317	0.3422	24.2597	211.04	25.245	504.81	12.1899	172.46	0.1371
Mo17xM0318	0.3196	24.1078	226.82	28.3102	613.4	13.1807	201.56	0.1405
Mo17xM0320	0.3386	25.1017	200.66	27.499	562.81	13.3526	191.24	0.1324
Mo17xM0321	0.3365	23.7427	184.14	22.4564	466.26	14.0385	165.76	0.1508
Mo17xM0322	0.2745	21.9468	184.22	22.4501	444.24	13.2676	145.56	0.1432
Mo17xM0323	0.2831	23.1006	193.52	20.552	497.6	12.7137	141.34	0.158
Mo17xM0324	0.3801	25.0391	204.35	26.7586	465.95	13.1675	177	0.1286
Mo17xM0325	0.3374	25.4245	216.29	29.9611	562.15	13.3857	193.15	0.1368
Mo17xM0326	0.2843	21.2186	154.91	16.3768	345.44	12.3541	102.9	0.1322
Mo17xM0327	0.3207	23.1472	208.03	20.6241	476.96	12.7731	154.47	0.1439

Figure 6S

Genotype	lsmean_ akw	lsmean_ cd	lsmean_ cl	lsmean_ cw	lsmean_ kc	lsmean_ krn	lsmean_ kw	lsmean_ sdw
Mo17xM0328	0.3446	22.805	177.03	21.9583	467.5	13.1784	158.9	0.1477
Mo17xM0331	0.3086	21.838	187.85	21.0543	453.29	13.883	158.72	0.1351
Mo17xM0334	0.3248	24.6775	203.97	26.2267	579.11	13.8672	185.92	0.1409
Mo17xM0335	0.336	22.497	206.48	23.7756	499.74	11.2078	168.25	0.1343
Mo17xM0337	0.3441	24.338	213.01	28.541	495.51	11.9915	175.75	0.1208
Mo17xM0338	0.3305	24.384	228.83	30.5782	598.69	12.1731	197.84	0.1625
Mo17xM0339	0.3821	26.9619	201.01	29.6669	615.26	14.642	235.9	0.1199
Mo17xM0341	0.3272	24.8741	168.88	22.3592	371.23	13.4186	122.3	0.1402
Mo17xM0342	0.3342	21.574	182.84	24.2378	454.11	14.0703	172.25	0.1561
Mo17xM0344	0.3592	24.624	218.52	28.4784	539.16	12.9433	196.03	0.1233
Mo17xM0345	0.3868	24.3021	227.58	28.8985	537.61	12.2641	207.71	0.1608
Mo17xM0348	0.3289	24.4905	214.56	25.4584	545.89	12.0301	180.14	0.1321
Mo17xM0350	0.3939	22.1549	206.24	24.0468	460.33	12.4214	181.42	0.1343
Mo17xM0351	0.3274	22.1026	162.03	17.9793	404.89	11.6408	136.17	0.1191
Mo17xM0352	0.3083	24.2631	207.97	24.9534	638.07	14.1846	198.83	0.1608
Mo17xM0353	0.3551	24.6846	216.24	27.2927	639.62	14.4101	226.97	0.1591
Mo17xM0354	0.355	21.5026	188.99	20.8015	409.67	12.1914	144.65	0.1235
Mo17xM0355	0.3494	23.5044	196.48	24.6689	536.63	13.2821	186.68	0.1186
Mo17xM0357	0.3264	23.2739	177.73	19.3384	384.34	12.688	127.12	0.1317
Mo17xM0358	0.329	25.4102	212.22	27.2323	575.86	14.5994	190.2	0.1272
Mo17xM0360	0.3028	22.7308	205.46	25.6925	490.32	12.0589	148.1	0.1382
Mo17xM0362	0.3843	25.7369	226.62	36.0326	595.87	13.7399	228.35	0.1465
Mo17xM0364	0.3343	23.7988	198.65	26.1046	556.53	13.7362	185.17	0.1537
Mo17xM0365	0.3485	25.1816	195.2	28.1743	538.92	14.0282	191.92	0.1362
Mo17xM0366	0.3338	23.0821	180.1	18.9818	472.59	12.7966	157.3	0.1476
Mo17xM0368	0.3831	25.9019	211.04	29.7047	547.24	13.147	208.26	0.1322
Mo17xM0369	0.3344	23.7374	220.27	26.2248	576.93	13.2868	193.09	0.1296
Mo17xM0370	0.3574	24.6293	184.96	25.7613	508.25	13.9135	187.37	0.1574
Mo17xM0375	0.371	23.6652	203.79	25.4794	512.89	12.6912	190.53	0.14
Mo17xM0376	0.3555	24.3997	226.46	30.1231	557.91	12.9427	203.62	0.1301
Mo17xM0377	0.3621	24.0699	194.84	24.4799	484.74	13.5269	177.86	0.1142
Mo17xM0378	0.3365	22.8859	190.13	21.3718	466.72	12.9485	155.69	0.1125
Mo17xM0379	0.3105	24.0738	200.18	23.2308	526.62	12.6729	163.86	0.1359
Mo17xM0380	0.3425	21.6762	168.44	21.1976	395.65	13.064	149.88	0.1398
Mo17xM0381	0.3474	24.4715	181.76	21.4922	496.9	12.9028	170.03	0.1301
Mo17xM0382	0.3159	22.583	183.84	21.0293	445.33	14.6411	145.98	0.1037
Mo17xM0383	0.3313	24.1445	191.45	29.2095	496.32	13.0567	164.1	0.1387
Mo17xM0384	0.3879	24.6045	212.83	27.0167	576.25	12.7924	220.24	0.1268
B73xM0040	NA	NA	NA	29.4686	NA	NA	NA	NA
M0040	NA	NA	NA	15.6327	NA	NA	NA	NA
Mo17xM0040	NA	NA	NA	29.0133	NA	NA	NA	NA
B73xM0042	NA	NA	NA	NA	NA	NA	NA	0.1277
B73xM0159	NA	NA	NA	NA	NA	NA	NA	0.1123
B73xM0221	NA	NA	NA	NA	NA	NA	NA	0.1057

Figure 6T

Genotype	lsmean_akw	lsmean_cd	lsmean_cl	lsmean_cw	lsmean_kc	lsmean_krn	lsmean_kw	lsmean_sdw
B73xM0237	NA	NA	NA	NA	NA	NA	NA	0.09759
B73xM0315	NA	NA	NA	NA	NA	NA	NA	0.08251
M0042	NA	NA	NA	NA	NA	NA	NA	0.05823
M0083	NA	NA	NA	NA	NA	NA	NA	0.1044
M0159	NA	NA	NA	NA	NA	NA	NA	0.1227
M0221	NA	NA	NA	NA	NA	NA	NA	0.09534
M0237	NA	NA	NA	NA	NA	NA	NA	0.08319
M0315	NA	NA	NA	NA	NA	NA	NA	0.06955
Mo17xM0042	NA	NA	NA	NA	NA	NA	NA	0.1388
Mo17xM0159	NA	NA	NA	NA	NA	NA	NA	0.1414
Mo17xM0221	NA	NA	NA	NA	NA	NA	NA	0.1267
Mo17xM0237	NA	NA	NA	NA	NA	NA	NA	0.1261
Mo17xM0315	NA	NA	NA	NA	NA	NA	NA	0.1559

Figure 6U

QTL REGULATING EAR PRODUCTIVITY TRAITS IN MAIZE

This application claims the benefit of U.S. Provisional Patent Application Ser. No. 61/364,104, filed Jul. 14, 2010, which is hereby incorporated by reference in its entirety.

FIELD OF THE INVENTION

This invention relates to quantitative trait loci regulating ear productivity traits in maize.

BACKGROUND OF THE INVENTION

Most plant traits of agronomic importance are polygenic, otherwise known as quantitative, traits. A quantitative trait is controlled by several genes located at various locations, or loci, in the plant's genome. The multiple genes have a cumulative effect which contributes to the continuous range of phenotypes observed in many plant traits. These genes are referred to as quantitative trait loci ("QTL").

Multiple experimental paradigms have been developed to identify and analyze QTL. In general, these paradigms involve crossing one or more parental pairs, which can be, for example, a single pair derived from two inbred strains, or multiple related or unrelated parents of different inbred strains or lines, which each exhibit different characteristics relative to the phenotypic trait of interest. The parents and a population of progeny are genotyped, typically for multiple marker loci, and evaluated for the trait of interest. QTL associated with traits of interest are identified based on the significant statistical correlations between the marker genotype(s) and the traits of interest phenotype of the evaluated progeny plants. Numerous methods for determining whether markers are genetically linked to a QTL (or to another marker) are known to those of skill in the art and include, e.g., interval mapping (Lander and Botstein, "Mapping Mendelian Factors Underlying Quantitative Traits Using RFLP Linkage Maps," *Genetics* 121:185-99 (1989)), regression mapping (Haley and Knott "A Simple Regression Method for Mapping Quantitative Trait Loci In Line Crosses Using Flanking Markers," *Heredity* 69:315-324 (1992)) or MQM mapping (Jansen, "Controlling the Type I and Type II Errors in Mapping Quantitative Trait Loci" *Genetics* 138: 871-881 (1994)).

Measurable traits related to ear productivity in maize include kernel row number ("KRN"), kernel count ("KC"), kernel weight ("KW"), average kernel weight ("AKW"), cob weight ("CW"), cob length ("CL"), cob diameter ("CD"), and seedling dry weight ("SDW"). These traits are considered quantitative traits and can be studied via QTL mapping. With this approach, genomic regions regulating a measurable trait are identified in populations segregating for the trait. See, e.g., Veldboom et al., "Molecular Marker-facilitated Studies In an Elite Maize Population: 1. Linkage Analysis and Determination of QTL for Morphological Traits," *Theor. Appl. Genet.* 88(1):7-16 (1994); Beavis et al., "Identification of Quantitative Trait Loci Using a Small Sample of Topcrossed and F4 Progeny from Maize," *Crop Sci.* 34:882-896 (1994); Austin et al., "Comparative Mapping in F-2:3 and F-6:7 Generations of Quantitative Trait Loci for Grain Yield and Yield Components In Maize," *Theor. Appl. Genet.* 92(7):817-826 (1996); Veldboom et al., "Genetic Mapping of Quantitative Trait Loci in Maize in Stress and Nonstress Environments. 1. Grain Yield and Yield Components," *Crop Sci.* 36(5):1310-1319 (1996); Veldboom et al., "Genetic Mapping of Quantitative Trait Loci in Maize in Stress and Nonstress Environments. 2. Plant Height and Flowering," *Crop Sci.* 36(5):1320-1327 (1996); Bommert et al., "Thick Tassel Dwarf1 Encodes a Putative Maize Ortholog of the *Arabidopsis* CLAVATA1 Leucine-rich Repeat Receptor-like Kinase," *Development* 132(6):1235-45 (2005); Tang et al., "Dissection of the Genetic Basis of Heterosis in an Elite Maize Hybrid by QTL Mapping In an Immortalized F2 Population," *Theor. Appl. Genet.* 120(2): 333-40 (2009).

A primary motivation for development of molecular markers in crop species is the potential for increased efficiency in plant breeding through marker assisted selection ("MAS"). Genetic marker alleles, or alternatively, identified QTL alleles, are used to identify plants that contain a desired genotype at one or more loci, and that are expected to transfer the desired genotype, along with a desired phenotype, to their progeny. Genetic marker alleles (or QTL alleles) can be used to identify plants that contain a desired genotype at one locus, or at several unlinked or linked loci (e.g., a haplotype), and that would be expected to transfer the desired genotype, along with a desired phenotype to their progeny.

Breeding, e.g., for increased ear productivity in maize via the traditional approach is difficult due to the multigenic nature of these traits. What is needed in the art is a means to identify genes conferring increased ear productivity using molecular markers. These markers can then be (i) used to tag the favorable alleles of these genes in segregating maize populations and (ii) employed to make selection for increased ear productivity more effective.

The present invention is directed to achieving these and other objectives and to overcoming limitations in the art.

SUMMARY OF THE INVENTION

One aspect of the present invention is directed to a method for determining an ear productivity trait in maize. This method involves analyzing genomic DNA from a maize plant, germplasm, pollen, or seed for the presence of a molecular marker linked to a QTL associated with an ear productivity trait in maize, where the molecular marker is selected from L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712.

Another aspect of the present invention is directed to a method of selecting a maize plant with a desired ear productivity trait. This method involves detecting in a maize plant, germplasm, seed, or pollen at least one allele of a marker locus that is associated with a desired ear productivity trait, where the one or more marker locus localizes within a chromosome interval defined by and including L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_

35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712. A maize plant with a desired ear productivity trait is selected by selecting the maize plant comprising the at least one allele of the marker locus.

A further aspect of the present invention is directed to a maize plant selected by methods of the present invention.

Another aspect of the present invention is directed to a method for reliably and predictably introgressing an improved ear productivity trait into a maize line. This method involves selecting plants for breeding based upon the presence of a molecular marker selected from L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712.

Another aspect of the present invention is directed to a method for producing a maize line having a desired ear productivity trait. This method involves providing a first maize line having a molecule marker selected from the group consisting of L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712, the molecular marker mapping to a genomic locus associated with a desired ear productivity trait. The desired ear productivity trait is introgressed into a maize line by selecting progeny plants for further breeding based upon the presence of the molecular marker to provide a recombinant maize line having the desired ear productivity trait.

A further aspect of the present invention is directed to a kit for selecting a maize plant by marker assisted selection of a QTL associated with a desired ear productivity trait. The kit includes primers for detecting at least one ear productivity trait marker locus selected from the group consisting of L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712. The kit also includes instructions for using the primers for detecting the ear productivity trait marker locus and correlating the locus with an improved ear productivity trait.

Another aspect of the present invention is directed to an isolated nucleic acid comprising a QTL associated with an ear productivity trait in maize. The QTL is proximal to a locus corresponding to a marker selected from the group consisting of L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712.

A further aspect of the present invention is directed to a transgenic plant comprising a recombinant nucleic acid genetically linked to a locus in maize, where the locus is proximal to a QTL associated with an ear productivity trait in a maize plant, and where the locus corresponds to a marker selected from the group consisting of L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712.

The present invention provides molecular markers genetically linked to QTL associated with ear productivity traits. The molecular markers are useful for identifying and producing maize plants with improved ear productivity traits.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** is a schematic illustration of a replicated greenhouse experiment according to a randomized design with constraints to position each recombinant inbred line ("RIL") and its corresponding hybrids (B73×RIL, Mo17×RIL) at neighboring positions within sand benches. Parental genotypes (B73, Mo17, F_1 hybrids) were distributed throughout each replication.

FIG. **2** is a schematic illustration showing a replicated field experiment design that was randomized with constraints to position each RIL and its corresponding hybrids (B73×RIL, Mo17×RIL) at equivalent positions within neighboring ranges. Parental genotypes (B73, Mo17, F_1 hybrids) were distributed throughout each replication.

Inbred and hybrid lines were contained in separate ranges to prevent shading and in-ground competition among inbred and hybrid lines.

FIGS. **3**A-B are tables identifying the context sequences of molecular markers of the present invention.

FIGS. **4**A-B are tables setting forth primer sequences for detecting the presence of molecular markers of the present invention.

FIGS. **5**A-D are tables identifying the context sequences of molecular markers of the present invention.

FIGS. **6**A-U are tables showing LS Means computed in SAS for each genotype and trait.

DETAILED DESCRIPTION OF THE INVENTION

One aspect of the present invention is directed to a method for determining an ear productivity trait in maize. This method involves analyzing genomic DNA from a maize plant, germplasm, pollen, or seed for the presence of a molecular marker linked to a QTL associated with an ear productivity trait in maize, where the molecular marker is selected from L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712.

Maize (*Zea mays* L.) is often referred to as corn in the United States. As used herein, a maize "plant" can be a whole plant, any part thereof, or a cell or tissue culture derived from a plant. Thus, the term "plant" can refer to any of whole plants, plant components or organs (e.g., leaves, stems, roots, etc.), plant tissues, seeds, plant cells, and/or progeny of the same. A plant cell is a cell of a plant, taken from a plant, or derived through culture from a cell taken from a plant.

Pursuant to the present invention, ear productivity traits may include, for example, measurable traits such as kernel row number (KRN), kernel count (KC), kernel weight (KW), average kernel weight (AKW), cob weight (CW), cob length (CL), cob diameter (CD), and seedling dry weight (SDW).

A QTL is a polymorphic genetic locus with at least two alleles that differentially affect the expression of a continuously distributed phenotypic trait, such as the measurable ear productivity traits described herein.

As used herein, a marker is a nucleotide sequence or encoded product thereof (e.g., a protein) used as a point of reference. For markers to be useful at detecting recombinations, they need to detect differences, or polymorphisms, within the population being monitored. For molecular markers, this means differences at the DNA level due to polynucleotide sequence differences (e.g., simple sequence repeats ("SSRs"), restriction fragment length polymorphisms ("RFLPs"), amplified fragment length polymorphisms ("AFLPs"), single nucleotide polymorphisms ("SNPs"). All markers are used to define a specific locus on the maize genome. Large numbers of these markers have been mapped. Each marker is therefore an indicator of a specific segment of DNA, having a unique nucleotide sequence. The map positions provide a measure of the relative positions of particular markers with respect to one another. When a trait is stated to be linked to a given marker it will be understood that the actual DNA segment whose sequence affects the trait generally co-segregates with the marker. More precise and definite localization of a trait can be obtained if markers are identified on both sides of the trait. By measuring the appearance of the marker(s) in progeny of crosses, the existence of the trait can be detected by relatively simple molecular tests without actually evaluating the appearance of the trait itself, which can be difficult and time-consuming because the actual evaluation of the trait requires growing plants to a stage where the trait can be expressed.

The genomic variability of a marker can be of any origin, for example, insertions, deletions, duplications, repetitive elements, point mutations, recombination events, or the presence and sequence of transposable elements. Molecular markers can be derived from genomic or expressed nucleic acids (e.g., ESTs) and can also refer to nucleic acids used as probes or primer pairs capable of amplifying sequence fragments via the use of PCR-based methods. A large number of maize molecular markers are known in the art, and are published or available from various sources.

In the context of the present invention, a QTL associated with an ear productivity trait means a nucleic acid and a phenotypic trait that are in linkage disequilibrium, i.e., the nucleic acid and the trait are found together in progeny plants more often than if the nucleic acid and phenotype segregated separately.

Recombination frequency measures the extent to which a molecular marker is linked with a QTL. Lower recombination frequencies, typically measured in centiMorgans ("cM"), indicate greater linkage between the QTL and the molecular marker. The extent to which two features are linked is often referred to as the genetic distance. The genetic distance is also typically related to the physical distance between the marker and the QTL. However, certain biological phenomenon (including recombinational "hot spots") can affect the relationship between physical distance and genetic distance. Generally, the usefulness of a molecular marker is determined by the genetic and physical distance between the marker and the selectable trait of interest. The linkage relationship between a molecular marker and a phenotype is given as a "probability" or "adjusted probability." Linkage can be expressed as a desired limit or range. For example, in some embodiments, any marker is linked (genetically and physically) to any other marker when the markers are separated by less than 50, 40, 30, 25, 20, or 15 map units (or cM). In some aspects, it is advantageous to define a bracketed range of linkage, for example, between 10 and 20 cM, between 10 and 30 cM, or between 10 and 40 cM. The more closely a marker is linked to a second locus, the better an indicator for the second locus that marker becomes. Thus, "closely linked loci" such as a marker locus and a second locus display an inter-locus recombination frequency of 10% or less, preferably about 9% or less, still more preferably about 8% or less, yet more preferably about 7% or less, still more preferably about 6% or less, yet more preferably about 5% or less, still more preferably about 4% or less, yet more preferably about 3% or less, and still more preferably about 2% or less. In highly preferred embodiments, the relevant loci display a recombination frequency of about 1% or less, e.g., about 0.75% or less, more preferably about 0.5% or less, or yet more preferably about 0.25% or less. Two loci that are localized to the same chromosome, and at such a distance that recombination between the two loci occurs at a frequency of less than 10% (e.g., about 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.75%, 0.5%, 0.25%, or less) are also said to be "proximal to" each other. Since one cM is the distance between two markers that show a 1% recombination frequency, any marker is closely linked (genetically and physically) to any other marker that is in close proximity, e.g., at or less than 10 cM distant. Two closely linked markers on the same chromosome can be positioned 9, 8, 7, 6, 5, 4, 3, 2, 1, 0.75, 0.5 or 0.25 cM or less from each other.

Data provided herein set forth a "logarithm of odds (LOD) value" or "LOD score" (Risch, "Genetic Linkage: Interpreting LOD Scores," *Science* 255:803-804 (1992), which is hereby incorporated by reference in its entirety). This is used in interval mapping to describe the degree of linkage between two marker loci. A LOD score of three (3.0) between two markers indicates that linkage is 1000 times more likely than no linkage, while a LOD score of two (2.0) indicates that linkage is 100 times more likely than no linkage. LOD scores greater than or equal to two (2.0) may be used to detect linkage.

According to the present invention, genomic DNA from a maize plant, germplasm, pollen, or seed is analyzed for the presence of a molecular marker linked to a QTL associated with an ear productivity trait in maize. Context DNA sequences for QTLs of the present invention are identified in the tables of FIGS. **3**A-B (SEQ ID NOs:1-39) and FIGS. **5**A-D (SEQ ID NOs:118-143). The complete genomic sequence of Maize has been published (Schnable et al., "The B73 Maize Genome: Complexity, Diversity and Dynamics," *Science* 326(5956):1112-1115 (2009), which is hereby incorporated by reference in its entirety) and may be helpful in carrying out the methods of the present invention. Analyzing genomic DNA from a maize plant, germplasm, pollen, or seed to determine the presence of a molecular marker corresponding to genetic polymorphisms between members of a population can be carried out by methods well-established in the art. These include, e.g., DNA sequencing, PCR-based sequence specific amplification methods, detection of RFLP, detection of isozyme markers, detection of polynucleotide polymorphisms by allele specific hybridization, detection of amplified variable sequences of the plant genome, detection of self-sustained sequence replication, detection of SSRs, detection of SNPs, or detection of AFLPs. Well-established methods are also known for the detection of expressed sequence tags ("ESTs") and SSR markers derived from EST sequences and randomly amplified polymorphic DNA.

The methods of the present invention may involve an automated system for detecting markers and/or correlating the markers with a desired phenotype (e.g., ear productivity). Thus, a typical system can include a set of marker probes or primers configured to detect at least one favorable allele of one or more marker locus associated with an ear productivity trait. These probes or primers are configured to detect the marker alleles described herein, e.g., using any available allele detection format, e.g., solid or liquid phase array based detection, microfluidic-based sample detection, etc.

The typical system includes a detector that is configured to detect one or more signal outputs from the set of marker probes or primers, or amplicon thereof, thereby identifying the presence or absence of the allele. A wide variety of signal detection apparatus are available, including photo multiplier tubes, spectrophotometers, CCD arrays, arrays and array scanners, scanning detectors, phototubes and photodiodes, microscope stations, galvo-scans, microfluidic nucleic acid amplification detection appliances, and the like. The precise configuration of the detector will depend, in part, on the type of label used to detect the marker allele, as well as the instrumentation that is most conveniently obtained for the user. Detectors that detect fluorescence, phosphorescence, radioactivity, pH, charge, absorbance, luminescence, temperature, magnetism or the like can be used. Typical detector examples include light (e.g., fluorescence) detectors or radioactivity detectors. For example, detection of a light emission (e.g., a fluorescence emission) or other probe label is indicative of the presence or absence of a marker allele. Fluorescent detection is generally used for detection of amplified nucleic acids (however, upstream and/or downstream operations can also be performed on amplicons, which can involve other detection methods). In general, the detector detects one or more label (e.g., light) emission from a probe label, which is indicative of the presence or absence of a marker allele.

The detector(s) optionally monitors one or a plurality of signals from an amplification reaction. For example, the detector can monitor optical signals which correspond to "real time" amplification assay results.

System instructions that correlate the presence or absence of the favorable allele with the predicted tolerance are also a feature of the invention. For example, the instructions can include at least one look-up table that includes a correlation between the presence or absence of the favorable alleles and the predicted ear productivity trait. The precise form of the instructions can vary depending on the components of the system, e.g., they can be present as system software in one or more integrated unit of the system (e.g., a microprocessor, computer or computer readable medium), or can be present in one or more units (e.g., computers or computer readable media) operably coupled to the detector. As noted, in one typical example, the system instructions include at least one look-up table that includes a correlation between the presence or absence of the favorable alleles and predicted tolerance or improved tolerance. The instructions also typically include instructions providing a user interface with the system, e.g., to permit a user to view results of a sample analysis and to input parameters into the system.

The system typically includes components for storing or transmitting computer readable data representing or designating the alleles detected by the methods of the present invention, e.g., in an automated system. The computer readable media can include cache, main, and storage memory and/or other electronic data storage components (hard drives, floppy drives, storage drives, etc.) for storage of computer code. Data representing alleles detected by the method of the present invention can also be electronically, optically, or magnetically transmitted in a computer data signal embodied in a transmission medium over a network such as an intranet or internet or combinations thereof. The system can also, or alternatively, transmit data via wireless, or other available transmission alternatives.

During operation, the system typically comprises a sample that is to be analyzed, such as a plant tissue, or material isolated from the tissue such as genomic DNA, amplified genomic DNA, cDNA, amplified cDNA, RNA, amplified RNA, or the like.

Automated systems for detecting markers and/or correlating the markers with a desired phenotype may involve data entering a computer which corresponds to physical objects or processes external to the computer, e.g., a marker allele, and a process that, within a computer, causes a physical transformation of the input signals to different output signals. In other words, the input data, e.g., amplification of a particular marker allele, is transformed to output data, e.g., the identification of the allelic form of a chromosome segment. The process within the computer is a set of instructions, or program, by which positive amplification or hybridization signals are recognized by the integrated system and attributed to individual samples as a genotype. Additional programs correlate the identity of individual samples with phenotypic values or marker alleles, e.g., statistical methods. In addition there are numerous e.g. C/C++ programs for computing, Delphi and/or Java programs for GUI interfaces, and productivity tools (e.g. Microsoft Excel and/or SigmaPlot) for charting or creating look up tables of relevant allele-trait correlations. Other useful software tools in the context of the integrated systems of the invention include statistical packages such as SAS, Genstat, Matlab, Mathematica, and S-Plus and genetic modeling packages such as QU-GENE. Furthermore, additional programming languages such as visual basic are also suitably employed in the integrated systems.

By way of example, ear productivity marker allele values assigned to a population of progeny descending from crosses between elite lines are recorded in a computer readable medium, thereby establishing a database corresponding tolerance alleles with unique identifiers for members of the population of progeny. Any file or folder, whether custom-made or commercially available (e.g., from Oracle or Sybase) suitable for recording data in a computer readable medium is acceptable as a database in the context of the present invention. Data regarding genotype for one or more molecular markers, e.g. SSR, RFLP, AFLP, SNP, isozyme markers or other markers as described herein, are similarly recorded in a computer accessible database. Optionally, marker data is obtained using an integrated system that automates one or more aspects of the assay (or assays) used to determine marker genotype. In such a system, input data corresponding to genotypes for molecular markers are relayed from a detector, e.g., an array, a scanner, a CCD, or other detection device directly to files in a computer readable medium accessible to the central processing unit. A set of system instructions (typically embodied in one or more programs) encoding the correlations between tolerance and the alleles of the invention is then executed by the computational device to identify correlations between marker alleles and predicted trait phenotypes.

Typically, the system also includes a user input device, such as a keyboard, a mouse, a touchscreen, or the like, for, e.g., selecting files, retrieving data, reviewing tables of maker information, etc., and an output device (e.g., a monitor, a printer, etc.) for viewing or recovering the product of the statistical analysis.

Integrated systems comprising a computer or computer readable medium comprising set of files and/or a database with at least one data set that corresponds to the marker alleles herein are provided. The system optionally also includes a user interface allowing a user to selectively view one or more of these databases. In addition, standard text manipulation software such as word processing software (e.g. MICROSOFT® Word or COREL® WORDPERFECT®) and database or spreadsheet software (e.g., spreadsheet software such as MICROSOFT® EXCEL®, COREL° QUATTRO PRO®, or database programs such as MICROSOFT® ACCESS® or PARADOX®) can be used in conjunction with a user interface (e.g., a GUI in a standard operating system such as a WINDOWS®, MACINTOSH®, UNIX®, or LINUX® systems) to manipulate strings of characters corresponding to the alleles or other features of the database.

The system may optionally include components for sample manipulation, e.g. incorporating robotic devices. For example, a robotic liquid control armature for transferring solutions (e.g., plant cell extracts) from a source to a destination, e.g., from a microtiter plate to an array substrate, is optionally operably linked to the digital computer (or to an additional computer in the integrated system). An input device for entering data to the digital computer to control high throughput liquid transfer by the robotic liquid control armature and, optionally, to control transfer by the armature to the solid support is commonly a feature of the integrated system. Many such automated robotic fluid handling systems are commercially available. For example, a variety of automated systems are available from Caliper Technologies (Hopkinton, Mass.), which utilize various Zymate systems, which typically include, e.g., robotics and fluid handling modules. Similarly, the common ORCA® robot, which is used in a variety of laboratory systems, e.g., for microtiter tray manipulation, is also commercially available, e.g., from Beckman Coulter, Inc. (Fullerton, Calif.). As an alternative to conventional robotics, microfluidic systems for performing fluid handling and detection are now widely available, e.g., from Caliper Technologies Corp. (Hopkinton, Mass.) and Agilent technologies (Palo Alto, Calif.).

Systems for molecular marker analysis can include a digital computer with one or more of high-throughput liquid control software, image analysis software for analyzing data from marker labels, data interpretation software, a robotic liquid control armature for transferring solutions from a source to a destination operably linked to the digital computer, an input device (e.g., a computer keyboard) for entering data to the digital computer to control high throughput liquid transfer by the robotic liquid control armature and, optionally, an image scanner for digitizing label signals from labeled probes hybridized, e.g., to markers on a solid support operably linked to the digital computer. The image scanner interfaces with the image analysis software to provide a measurement of, e.g., nucleic acid probe label intensity upon hybridization to an arrayed sample nucleic acid population (e.g., comprising one or more markers), where the probe label intensity measurement is interpreted by the data interpretation software to show whether, and to what degree, the labeled probe hybridizes to a marker nucleic acid (e.g., an amplified marker allele). The data so derived is then correlated with sample identity, to determine the identity of a plant with a particular genotype(s) for particular markers or alleles, e.g., to facilitate marker assisted selection of maize plants with favorable allelic forms of chromosome segments involved in agronomic performance (e.g., ear productivity traits).

Optical images, e.g., hybridization patterns viewed (and, optionally, recorded) by a camera or other recording device (e.g., a photodiode and data storage device) are optionally further processed in any of the embodiments herein, e.g., by digitizing the image and/or storing and analyzing the image on a computer. A variety of commercially available peripheral equipment and software is available for digitizing, storing, and analyzing a digitized video or digitized optical image, e.g., using PC (INTEL® x86 or PENTIUM® chip-compatible MS-DOS®, OS/2®, WINDOWS®, WINDOWS® NT or WINDOWS® 95 based machines), MACINTOSH®, LINUX®, or UNIX® based (e.g. SUN® work station) computers.

According to one embodiment, the ear productivity trait is kernel row number (KRN) and the marker is selected from L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_77055, SNP_81248, SNP_82913, SNP_90380, SNP_11948, SNP_61221, SNP_70805, SNP_94161, SNP_2880, and SNP_36300.

In another embodiment, the ear productivity trait is cob weight (CW) and the marker is selected from SNP_98111, SNP_32823, SNP_4623, SNP_90941, SNP_27764, SNP_95039, SNP_75795, SNP_34738, and SNP_77712.

In yet another embodiment, the ear productivity trait is cob diameter (CD) and the marker is selected from SNP_90941, SNP_82913, SNP_93907, SNP_105143, SNP_43846, SNP_98032, SNP_88270, and SNP_77712.

In still another embodiment, the ear productivity trait is cob length (CL) and the marker is selected from SNP_35511, SNP_19249, and SNP_49724.

In another embodiment, the ear productivity trait is kernel weight (KW) and the marker is selected from SNP_79262, SNP_9084, and SNP_84372.

In yet another embodiment, the ear productivity trait is kernel count (KC) and the marker is selected from SNP_9084, SNP_99055, SNP_45551, SNP_89298_2, SNP_51496, and SNP_63437.

In addition to the markers identified herein, other markers linked to the markers described herein can be used to predict ear productivity in a maize plant and are therefore also useful in carrying out the methods of the present invention. This includes any marker within, e.g., 50 cM of the markers associated with ear productivity at a p-level ≤0.01 in the association analysis. The closer a marker is to a gene controlling a trait of interest, the more effective and advantageous that marker is as an indicator for the desired trait. Closely linked loci display an inter-locus cross-over frequency of about 10% or less, preferably about 9% or less, still more preferably about 8% or less, yet more preferably about 7% or less, still more preferably about 6% or less, yet more preferably about 5% or less, still more preferably about 4% or less, yet more preferably about 3% or less, and still more preferably about 2% or less. In highly preferred embodiments, the relevant loci (e.g., a marker locus and a target locus) display a recombination frequency of about 1% or less, e.g., about 0.75% or less, more preferably about 0.5% or less, or yet more preferably about 0.25% or less. Thus, the loci are about 10 cM, 9 cM, 8 cM, 7 cM, 6 cM, 5 cM, 4 cM, 3 cM, 2 cM, 1 cM, 0.75 cM, 0.5 cM or 0.25 cM or less apart.

After a desired phenotype and a polymorphic chromosomal locus, e.g., a marker locus or QTL, are determined to segregate together, it is possible to use those polymorphic loci to select for alleles corresponding to the desired phenotype—a process called marker-assisted selection ("MAS"). In brief, a nucleic acid corresponding to the marker nucleic acid is detected in a biological sample from a plant to be selected. This detection can take the from of hybridization of a probe nucleic acid to a marker, e.g., using allele-specific hybridization, Southern analysis, northern analysis, in situ hybridization, hybridization of primers followed by PCR amplification of a region of the marker, or the like. A variety of procedures for detecting markers are described herein. After the presence (or absence) of a particular marker in the biological sample is verified, the plant is selected, i.e., used to make progeny plants by selective breeding.

Although particular marker alleles can show co-segregation with increased ear productivity, the marker locus is not necessarily responsible for the expression of ear productivity phenotypes. For example, it is not a requirement that the marker polynucleotide sequence be part of a gene that imparts increased ear productivity (for example, be part of the gene open reading frame). The association between a specific marker allele and a particular ear productivity phenotype is due to the original "coupling" linkage phase between the marker allele and the allele in the ancestral maize line from which the allele originated. Eventually, with repeated recombination, crossing over events between the marker and genetic locus can change this orientation. For this reason, the favorable marker allele may change depending on the linkage phase that exists within the parent used to create segregating populations. This does not change the fact that the marker can be used to monitor segregation of the phenotype. It only changes which marker allele is considered favorable in a given segregating population. Chromosomal intervals (i.e. any and all intervals defined by any of the markers of the present invention) that correlate with ear productivity are provided herein.

A variety of methods well known in the art are available for identifying chromosomal intervals. The boundaries of such chromosomal intervals are drawn to encompass markers that will be linked to the gene controlling the trait of interest. In other words, the chromosomal interval is drawn such that any marker that lies within that interval (including the terminal markers that define the boundaries of the interval) can be used as a marker for ear productivity traits. The intervals described herein are set forth in Tables 2 and 4, and encompass markers that co-segregate with ear productivity traits. The clustering of markers occurs in relatively small domains on the chromosomes, indicating the presence of a gene controlling the trait of interest in those chromosome regions.

Maize breeders desire combinations of desirable traits to develop improved maize varieties. Screening large numbers of samples by non-molecular methods (e.g., trait evaluation in maize plants) can be expensive, time consuming, and unreliable. Use of the polymorphic markers described herein genetically linked to ear productivity loci provide effective methods for selecting high-yielding varieties in breeding programs. For example, one advantage of marker-assisted selection over field evaluations is that MAS can be done at any time of year, regardless of the growing season. Moreover, environmental effects are largely irrelevant to marker-assisted selection.

When a plant population is segregating for multiple loci affecting one or multiple traits, e.g., multiple loci involved in ear productivity, or multiple loci each involved in ear productivity, the efficiency of MAS compared to phenotypic screening becomes even greater, because all of the loci can be evaluated in the lab together from a single sample of DNA. In the present invention, markers of the present invention can be assayed simultaneously or sequentially in a single sample or population of samples.

Thus, another aspect of the present invention is directed to a method of selecting a maize plant with desired ear productivity trait. This method involves detecting in a maize plant, germplasm, seed, or pollen at least one allele of a marker locus that is associated with a desired ear productivity trait, where the one or more marker locus localizes within a chromosome interval defined by and including L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712. A maize plant with a desired ear productivity trait is selected by selecting the maize plant comprising the at least one allele of the marker locus.

In one embodiment, selecting the maize plant pursuant to this method of the present invention occurs as part of a breeding program to improve a maize variety's ear productivity. Breeding programs are well-known in the art and may include, e.g., crossing, making hybrids, backcrossing, self-crossing, double haploid breeding, and/or combinations thereof.

Field crops are bred through techniques that take advantage of the plant's method of pollination. A plant is self-pollinated if pollen from one flower is transferred to the same or another flower of the same plant. A plant is sib pollinated when individuals within the same family or line are used for pollination. A plant is cross-pollinated if the pollen comes from a flower on a different plant from a different family or line.

Plants that have been self-pollinated and selected for type for many generations become homozygous at almost all gene loci and produce a uniform population of true breeding progeny. A cross between two different homozygous lines produces a uniform population of hybrid plants that may be heterozygous for many gene loci. A cross of two plants each heterozygous at a number of gene loci will produce a population of heterogeneous plants that differ genetically and will not be uniform.

Maize can be bred by both self-pollination (self-crossing) and cross-pollination (crossing) techniques. Maize has separate male and female flowers on the same plant, located on the tassel and the ear, respectively.

Crossing means the fusion of gametes via pollination to produce progeny (i.e., cells, seeds, or plants). The term encompasses both sexual crosses (the pollination of one plant by another) and selfing (self-pollination, i.e., when the pollen and ovule are from the same plant). Natural pollination occurs in maize when wind blows pollen from the tassels to the silks that protrude from the tops of the ears. Large scale commercial maize hybrid production, as it is practiced today, requires the use of some form of male sterility system which controls or inactivates male fertility. A reliable method of controlling male fertility in plants also offers the opportunity for improved plant breeding. This is especially true for development of maize hybrids, which relies upon some sort of male sterility system. There are several ways in which a maize plant can be manipulated so that is male sterile. These include use of manual or mechanical emasculation (or detasseling), cytoplasmic genetic male sterility, nuclear genetic male sterility, gametocides and the like, which are discussed infra.

The development of a hybrid maize variety in a maize plant breeding program involves three steps: (1) the selection of plants from various germplasm pools for initial breeding crosses; (2) the selfing of the selected plants from the breeding crosses for several generations to produce a series of inbred lines, which, individually breed true and are highly uniform; and (3) crossing a selected inbred line with an unrelated inbred line to produce the hybrid progeny (F_1). After a sufficient amount of inbreeding, successive filial generations will merely serve to increase seed of the developed inbred. Preferably, an inbred line should comprise homozygous alleles at about 95% or more of its loci.

As noted above, hybrid maize seed is often produced by a male sterility system incorporating manual or mechanical detasseling. By way of example, alternate strips of two inbred varieties of maize can be planted in a field, and the pollen-bearing tassels removed from one of the inbreds (female) prior to pollen shed. Provided that there is sufficient isolation from sources of foreign maize pollen, the ears of the detasseled inbred will be fertilized only from the other inbred (male), and the resulting seed is therefore hybrid and will form hybrid plants.

The laborious detasseling process can be avoided by using cytoplasmic malesterile ("CMS") inbreds. Plants of a CMS inbred are male sterile as a result of factors resulting from the cytoplasmic, as opposed to the nuclear, genome. Thus, this characteristic is inherited exclusively through the female parent in maize plants, since only the female provides cytoplasm to the fertilized seed. CMS plants are fertilized with pollen from another inbred that is not male-sterile. Pollen from the second inbred may or may not contribute genes that make the hybrid plants male-fertile. The same hybrid seed, a portion produced from detasseled fertile maize and a portion produced using the CMS system can be blended to insure that adequate pollen loads are available for fertilization when the hybrid plants are grown.

There are several methods of conferring genetic male sterility available, such as multiple mutant genes at separate locations within the genome that confer male sterility, as disclosed in U.S. Pat. Nos. 4,654,465 and 4,727,219 to Brar et al., which are hereby incorporated by reference in their entirety, and chromosomal translocations as described in U.S. Pat. Nos. 3,861,709 and 3,710,511 to Patterson, which are hereby incorporated by reference in their entirety. In addition to these methods, U.S. Pat. No. 5,432,068 to Albertsen et al., which is hereby incorporated by reference in its entirety, describes a system of nuclear male sterility which includes: identifying a gene which is critical to male fertility; silencing this native gene which is critical to male fertility; removing the native promoter from the essential male fertility gene and replacing it with an inducible promoter; inserting this genetically engineered gene back into the plant; and thus creating a plant that is male sterile because the inducible promoter is not "on" resulting in the male fertility gene not being transcribed. Fertility is restored by inducing, or turning "on" the promoter, which in turn allows the gene that confers male fertility to be transcribed.

There are many other methods of conferring genetic male sterility in the art, each with its own benefits and drawbacks. These methods use a variety of approaches such as delivering into the plant a gene encoding a cytotoxic substance associated with a male tissue specific promoter or an antisense system in which a gene critical to fertility is identified and an antisense to that gene is inserted in the plant. See, e.g., PCT Publication No. WO 90/08828 to Fabinjanski et al., which is hereby incorporated by reference in its entirety.

The use of male sterile inbreds is but one factor in the production of maize hybrids. The development of maize hybrids in a maize plant breeding program requires, in general, the development of homozygous inbred lines, the crossing of these lines, and the evaluation of the crosses. Maize plant breeding programs combine the genetic backgrounds from two or more inbred lines or various other germplasm sources into breeding populations from which new inbred lines are developed by selfing and selection of desired phenotypes. Hybrids also can be used as a source of plant breeding material or as source populations from which to develop or derive new maize lines. Plant breeding techniques known in the art and used in a maize plant breeding program include, but are not limited to, recurrent selection, backcrossing, double haploids, pedigree breeding, restriction fragment length polymorphism enhanced selection, genetic marker enhanced selection, and transformation. Often a combination of these techniques are used. The inbred lines derived from hybrids can be developed using plant breeding techniques as described herein. New inbreds are crossed with other inbred lines and the hybrids from these crosses are evaluated to determine which of those have commercial potential.

Backcrossing refers to the process whereby hybrid progeny are repeatedly crossed back to one of the parents. In a backcrossing scheme, the "donor" parent refers to the parental plant with the desired gene or locus to be introgressed. The "recipient" parent (used one or more times) or "recurrent" parent (used two or more times) refers to the parental plant into which the gene or locus is being introgressed. For example, see Ragot et al., "Marker-assisted Backcrossing: A Practical Example," *Techniques et Utilisations des Marqueurs Moleculaires Les Colloques*, vol. 72, pp. 45-56 (1995) and Openshaw et al., "Marker-assisted Selection in Backcross Breeding," *Analysis of Molecular Marker Data*, pp. 41-43 (1994), which are hereby incorporated by reference in their entirety. The initial cross gives rise to the F_1 generation; the term "BC1" then refers to the second use of the recurrent parent, "BC2" refers to the third use of the recurrent parent, and so on.

Backcrossing can be used to improve inbred lines and a hybrid which is made using those inbreds. Backcrossing can be used to transfer a specific desirable trait from one line, the donor parent, to an inbred called the recurrent parent which has overall good agronomic characteristics yet that lacks the desirable trait. This transfer of the desirable trait into an inbred line with overall good agronomic characteristics can be accomplished by first crossing a recurrent parent to a donor parent (non-recurrent parent). The progeny of this cross is then mated back to the recurrent parent followed by selection in the resultant progeny for the desired trait to be transferred from the non-recurrent parent. Typically after four or more backcross generations with selection for the desired trait, the progeny will contain essentially all genes of the recurrent parent except for the genes controlling the desired trait. But the number of backcross generations can be less if molecular markers are used during the selection or elite germplasm is used as the donor parent. The last backcross generation is then selfed to give pure breeding progeny for the gene(s) being transferred.

Backcrossing can also be used in conjunction with pedigree breeding to develop new inbred lines. For example, an F_1 can be created that is backcrossed to one of its parent lines to create a BC1. Progeny are selfed and selected so that the newly developed inbred has many of the attributes of the recurrent parent and some of the desired attributes of the non-recurrent parent.

Recurrent selection is a method used in a plant breeding program to improve a population of plants. The method entails individual plants cross pollinating with each other to form progeny which are then grown. The superior progeny are then selected by any number of methods, which include individual plant, half sib progeny, full sib progeny, selfed progeny, and topcrossing. The selected progeny are cross pollinated with each other to form progeny for another population. This population is planted and again superior plants are selected to cross pollinate with each other. Recurrent selection is a cyclical process and, therefore, can be repeated as many times as desired. The objective of recurrent selection is to improve the traits of a population. The improved population can then be used as a source of breeding material to obtain inbred lines to be used in hybrids or used as parents for a synthetic cultivar. A synthetic cultivar is the resultant progeny formed by the intercrossing of several selected inbreds. Mass selection is a useful technique when used in conjunction with molecular marker enhanced selection.

The production of double haploids can also be used in a breeding program. Double haploids are produced by the doubling of a set of chromosomes (1N) from a heterozygous plant to produce a completely homozygous individual. See, e.g., Wan et al., "Efficient Production of Doubled Haploid Plants Through Colchicine Treatment of Anther-Derived Maize Callus." *Theoretical and Applied Genetics* 77:889-892 (1989) and U.S. Patent Application Publication No. 2003/0005479, which are hereby incorporated by reference in their entirety. This can be advantageous because the process omits the generations of selfing needed to obtain a homozygous plant from a heterozygous source. Double haploid breeding methods may be used at any step in a breeding process. For example, instead of selfing out of the hybrid produced from the inbred, one could first cross the hybrid to either a parent line or a different inbred, and then self out of that cross.

A further aspect of the present invention is directed to a maize plant selected pursuant to the methods of the present invention.

Marker loci of the present invention can be introgressed into any desired genomic background, germplasm, plant, line, variety, etc., as part of an overall MAS breeding program designed to enhance maize yield, or for any other purpose. Thus, another aspect of the present invention is directed to a method for reliably and predictably introgressing an improved ear productivity trait into a maize line. This method involves selecting plants for breeding based upon the presence of a molecular marker selected from L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712.

Introgression refers to the transmission of a desired allele of a genetic locus from one genetic background to another. For example, introgression of a desired allele at a specified locus can be transmitted to at least one progeny plant via a sexual cross between two parent plants, where at least one of the parent plants has the desired allele within its genome. Alternatively, for example, transmission of an allele can occur by recombination between two donor genomes, e.g., in a fused protoplast, where at least one of the donor protoplasts has the desired allele in its genome. The desired allele can be, e.g., a transgene or a selected allele of a marker or QTL.

Offspring possessing the desired allele can be repeatedly backcrossed to a line having a desired genetic background and selected for the desired allele, to result in the allele becoming fixed in a selected genetic background. For example, markers described herein may be introgressed into a recurrent parent. The recurrent parent line with the introgressed gene or locus may then have a desired ear productivity trait.

Another aspect of the present invention is directed to a method for producing a maize line having a desired ear productivity trait. This method involves providing a first maize line having a molecule marker selected from the group consisting of L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712, the molecular marker mapping to a genomic locus associated with a desired ear productivity trait. The desired ear productivity trait is introgressed into a maize line by selecting progeny plants for further breeding based upon the presence of the molecular marker to provide a recombinant maize line having the desired ear productivity trait.

Another aspect of the present invention is directed to a kit for selecting a maize plant by marker assisted selection of a QTL associated with a desired ear productivity trait. The kit includes primers for detecting at least one ear productivity trait marker locus selected from the group consisting of L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712. The kit also includes instructions for using the primers for detecting the ear productivity trait marker locus and correlating the locus with an improved ear productivity trait.

Suitable primers for detecting ear productivity trait marker loci of the present invention can be generated from the sequence data provided in FIGS. **3**A-B and FIGS. **5**A-D. In one embodiment, primers are selected from those set forth in FIGS. **4**A-B.

Another aspect of the present invention is directed to an isolated nucleic acid comprising a QTL associated with an ear productivity trait in maize. The QTL is proximal to a locus corresponding to a marker selected from the group consisting of L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712.

A further aspect of the present invention is directed to a transgenic plant comprising a recombinant nucleic acid genetically linked to a locus in maize, where the locus is proximal to a QTL associated with an ear productivity trait in a maize plant, and where the locus corresponds to a marker selected from the group consisting of L00401, L004011 c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712.

Methods of producing recombinant nucleic acids for purposes of making transgenic plants are well-known. In one embodiment, the present invention utilizes recombinant nucleic acid sequences that are genetically linked to a locus in maize, where the locus is proximal to a QTL associated with an ear productivity trait. The locus corresponds to one or more of the markers described herein. Nucleic acid sequences for making transgenic plants according to the present invention may be inserted into any of the many available expression vectors and cell systems using reagents that are well known in the art. Suitable vectors include, but are not limited to, the following viral vectors such as lambda vector system gt11, gt WES.tB, Charon 4, and plasmid vectors such as pBI121, pBI525, pG-Cha, p35S-Cha, pBR322, pBR325, pACYC177, pACYC1084, pUC8, pUC9, pUC18, pUC19, pLG339, pR290, pKC37, pKC101, SV 40, pBluescript II SK +/− or KS +/− (see "Stratagene Cloning Systems" Catalog (1993) from Stratagene, La Jolla, Calif., which is hereby incorporated by reference in its entirety), pQE, pIH821, pGEX, pET series (see Studier et al., "Use of T7 RNA Polymerase to Direct Expression of Cloned Genes," *Gene Expression Technology vol.* 185 (1990), which is hereby incorporated by reference in its entirety), and any derivatives thereof.

Recombinant molecules can be introduced into cells via transformation, particularly transduction, conjugation, mobilization, or electroporation. The DNA sequences are cloned into the vector using standard cloning procedures in the art, as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, N.Y., Cold Spring Harbor Press (1989), and Ausubel et al., *Current*

Protocols in Molecular Biology, New York, N.Y., John Wiley & Sons (1989), which are hereby incorporated by reference in their entirety.

In preparing a nucleic acid vector for expression, the various nucleic acid sequences may normally be inserted or substituted into a bacterial plasmid. Any convenient plasmid may be employed, which will be characterized by having a bacterial replication system, a marker which allows for selection in a bacterium, and generally one or more unique, conveniently located restriction sites. Numerous plasmids, referred to as transformation vectors, are available for plant transformation. The selection of a vector will depend on the preferred transformation technique. A variety of vectors are available for stable transformation using *Agrobacterium tumefaciens*, a soilborne bacterium that causes crown gall. Crown gall are characterized by tumors or galls that develop on the lower stem and main roots of the infected plant. These tumors are due to the transfer and incorporation of part of the bacterium plasmid DNA into the plant chromosomal DNA. This transfer DNA ("T-DNA") is expressed along with the normal genes of the plant cell. The plasmid DNA, pTi, or Ti-DNA, for "tumor inducing plasmid," contains the vir genes necessary for movement of the T-DNA into the plant. The T-DNA carries genes that encode proteins involved in the biosynthesis of plant regulatory factors, and bacterial nutrients (opines). The T-DNA is delimited by two 25 bp imperfect direct repeat sequences called the "border sequences." By removing the oncogene and opine genes, and replacing them with a gene of interest, it is possible to transfer foreign DNA into the plant without the formation of tumors or the multiplication of *Agrobacterium tumefaciens* (Fraley et al., "Expression of Bacterial Genes in Plant Cells," *Proc. Nat'l Acad. Sci.* 80:4803-4807 (1983), which is hereby incorporated by reference in its entirety).

Further improvement of this technique led to the development of the binary vector system (Bevan, "Binary *Agrobacterium* Vectors for Plant Transformation," *Nucleic Acids Res.* 12:8711-8721 (1984), which is hereby incorporated by reference in its entirety). In this system, all the T-DNA sequences (including the borders) are removed from the pTi, and a second vector containing T-DNA is introduced into *Agrobacterium tumefaciens*. This second vector has the advantage of being replicable in *E. coli* as well as *A. tumefaciens*, and contains a multiclonal site that facilitates the cloning of a transgene. An example of a commonly-used vector is pBin19 (Frisch et al., "Complete Sequence of the Binary Vector Bin19," *Plant Molec. Biol.* 27:405-409 (1995), which is hereby incorporated by reference in its entirety). Any appropriate vectors now known or later described for genetic transformation are suitable for use with the present invention.

U.S. Pat. No. 4,237,224 to Cohen and Boyer, which is hereby incorporated by reference in its entirety, describes the production of expression systems in the form of recombinant plasmids using restriction enzyme cleavage and ligation with DNA ligase. These recombinant plasmids are then introduced by means of transformation and replicated in unicellular cultures including prokaryotic organisms and eukaryotic cells grown in tissue culture.

Certain "control elements" or "regulatory sequences" are also incorporated into the vector-construct. These include non-translated regions of the vector, promoters, and 5' and 3' untranslated regions which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. Tissue-specific and organ-specific promoters can also be used.

A constitutive promoter is a promoter that directs expression of a gene throughout the development and life of an organism. Examples of some constitutive promoters that are widely used for inducing expression of transgenes include the nopaline synthase ("NOS") gene promoter, from *Agrobacterium tumefaciens* (U.S. Pat. No. 5,034,322 to Rogers et al., which is hereby incorporated by reference in its entirety), the cauliflower mosaic virus (CaMV) 35S and 19S promoters (U.S. Pat. No. 5,352,605 to Fraley et al., which is hereby incorporated by reference in its entirety), those derived from any of the several actin genes, which are known to be expressed in most cells types (U.S. Pat. No. 6,002,068 to Privalle et al., which is hereby incorporated by reference in its entirety), and the ubiquitin promoter, which is a gene product known to accumulate in many cell types.

An inducible promoter is a promoter that is capable of directly or indirectly activating transcription of one or more DNA sequences or genes in response to an inducer. In the absence of an inducer, the DNA sequences or genes will not be transcribed. The inducer can be a chemical agent, such as a metabolite, growth regulator, herbicide, or phenolic compound, or a physiological stress directly imposed upon the plant such as cold, heat, salt, toxins, or through the action of a pathogen or disease agent such as a virus or fungus. A plant cell containing an inducible promoter may be exposed to an inducer by externally applying the inducer to the cell or plant such as by spraying, watering, heating, or by exposure to the operative pathogen. An example of an appropriate inducible promoter is a glucocorticoid-inducible promoter (Schena et al., "A Steroid-Inducible Gene Expression System for Plant Cells," *Proc. Natl. Acad. Sci.* 88:10421-5 (1991), which is hereby incorporated by reference in its entirety). Expression of the transgene-encoded protein is induced in the transformed plants when the transgenic plants are brought into contact with nanomolar concentrations of a glucocorticoid, or by contact with dexamethasone, a glucocorticoid analog (Schena et al., "A Steroid-Inducible Gene Expression System for Plant Cells," *Proc. Natl. Acad. Sci. USA* 88:10421-5 (1991); Aoyama et al., "A Glucocorticoid-Mediated Transcriptional Induction System in Transgenic Plants," *Plant J.* 11:605-612 (1997); and McNellis et al., "Glucocorticoid-Inducible Expression of a Bacterial Avirulence Gene in Transgenic *Arabidopsis* Induces Hypersensitive Cell Death," *Plant J.* 14(2):247-57 (1998), which are hereby incorporated by reference in their entirety). In addition, inducible promoters include promoters that function in a tissue specific manner to regulate the gene of interest within selected tissues of the plant. Examples of such tissue specific or developmentally regulated promoters include seed, flower, fruit, or root specific promoters as are well known by those of ordinary skill in the art (U.S. Pat. No. 5,750,385 to Shewmaker et al., which is hereby incorporated by reference in its entirety).

A number of tissue- and organ-specific promoters have been developed for use in genetic engineering of plants (Potenza et al., "Targeting Transgene Expression in Research, Agricultural, and Environmental Applications: Promoters Used in Plant Transformation," *In Vitro Cell. Dev. Biol. Plant* 40:1-22 (2004), which is hereby incorporated by reference in its entirety). Examples of such promoters include those that are floral-specific (Annadana et al., "Cloning of the Chrysanthemum UEP1 Promoter and Comparative Expression in Florets and Leaves of *Dendranthema grandiflora," Transgenic Res.* 11:437-445 (2002), which is hereby incorporated by reference in its entirety), seed-specific (Kluth et al., "5' Deletion of a gbss1 Promoter Region Leads to Changes in Tissue and Developmental Specificities," *Plant Mol. Biol.* 49:669-682 (2002), which is hereby incorporated by reference in its entirety), root-specific (Yamamoto et al., "Characterization of cis-acting Sequences Regulating Root-Specific Gene Expression in Tobacco," *Plant Cell* 3:371-382 (1991), which is hereby incorporated by reference in its entirety), fruit-specific (Fraser et al., "Evaluation of Transgenic Tomato Plants Expressing an Additional Phytoene Synthase in a Fruit-Specific Manner," *Proc. Natl. Acad. Sci. USA* 99:1092-1097 (2002), which is hereby incorporated by reference in its entirety), and tuber/storage organ-specific (Visser et al., "Expression of a Chimaeric Granule-Bound Starch Synthase-GUS Gene in Transgenic Potato Plants," *Plant Mol. Biol.* 17:691-699 (1991), which is hereby incorporated by reference in its entirety). Targeted expression of an introduced gene (transgene) is necessary when expression of the transgene could have detrimental effects if expressed throughout the plant. On the other hand, silencing a gene throughout a plant could also have negative effects. However, this problem could be avoided by localizing the silencing to a region by a tissue-specific promoter.

Nucleic acid constructs of the present invention include an operable 3' regulatory region, selected from among those which are capable of providing correct transcription termination and polyadenylation of mRNA for expression in the host cell of choice, operably linked to a nucleic acid molecule configured to silence BBTV. A number of 3' regulatory regions are known to be operable in plants. Exemplary 3' regulatory regions include, without limitation, the nopaline synthase ("nos") 3' regulatory region (Fraley et al., "Expression of Bacterial Genes in Plant Cells," *Proc. Nat'l Acad. Sci. USA* 80:4803-4807 (1983), which is hereby incorporated by reference in its entirety) and the cauliflower mosaic virus ("CaMV") 3' regulatory region (Odell et al., "Identification of DNA Sequences Required for Activity of the Cauliflower Mosaic Virus 35S Promoter," *Nature* 313(6005):810-812 (1985), which is hereby incorporated by reference in its entirety). Virtually any 3' regulatory region known to be operable in plants would be suitable for use in conjunction with the present invention.

The different components described supra can be ligated together to produce the expression systems which contain the nucleic acid constructs of the present invention, using well known molecular cloning techniques as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition Cold Spring Harbor, N.Y., Cold Spring Harbor Press (1989), and Ausubel et al. *Current Protocols in Molecular Biology*, New York, N.Y., John Wiley & Sons (1989), which are hereby incorporated by reference in their entirety.

Once the nucleic acid construct of the present invention has been prepared, it is ready to be incorporated into a host cell. Accordingly, another aspect of the present invention relates to a recombinant host cell containing one or more of the nucleic acid constructs of the present invention. Basically, this method is carried out by transforming a host cell with a nucleic acid construct of the present invention under conditions effective to achieve transcription of the nucleic acid molecule in the host cell. This is achieved with standard cloning procedures known in the art, such as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Springs Laboratory, Cold Springs Harbor, N.Y. (1989), which is hereby incorporated by reference in its entirety. Suitable host cells include, but are not limited to, bacteria, virus, yeast, mammalian cells, insect, plant, and the like. Preferably the host cells are either a bacterial cell or a plant cell. Methods of transformation may result in transient or stable expression of the nucleic acid under control of the promoter. Preferably, a nucleic acid construct of the present invention is stably inserted into the genome of the recombinant plant cell as a result of the transformation, although transient expression can serve an important purpose.

Plant tissue suitable for transformation includes leaf tissue, root tissue, meristems, zygotic and somatic embryos, callus, protoplasts, tassels, pollen, embryos, anthers, and the like. The means of transformation chosen is that most suited to the tissue to be transformed.

Transient expression in plant tissue can be achieved by particle bombardment (Klein et al., "High-Velocity Microprojectiles for Delivering Nucleic Acids Into Living Cells," *Nature* 327:70-73 (1987), which is hereby incorporated by reference in its entirety), also known as biolistic transformation of the host cell, as disclosed in U.S. Pat. Nos. 4,945,050; 5,036,006; and 5,100,792, all to Sanford et al., and in Emerschad et al., "Somatic Embryogenesis and Plant Development from Immature Zygotic Embryos of Seedless Grapes (*Vitis vinifera*)," *Plant Cell Reports* 14:6-12 (1995), which are hereby incorporated by reference in their entirety.

In particle bombardment, tungsten or gold microparticles (1 to 2 μm in diameter) are coated with the DNA of interest and then bombarded at the tissue using high pressure gas. In this way, it is possible to deliver foreign DNA into the nucleus and obtain a temporal expression of the gene under the current conditions of the tissue. Biologically active particles (e.g., dried bacterial cells containing the vector and heterologous DNA) can also be propelled into plant cells. Other variations of particle bombardment, now known or hereafter developed, can also be used.

An appropriate method of stably introducing the nucleic acid construct into plant cells is to infect a plant cell with *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes* previously transformed with the nucleic acid construct of the present invention. As described supra, the Ti (or R1) plasmid of *Agrobacterium* enables the highly successful transfer of a foreign nucleic acid molecule into plant cells. A variation of *Agrobacterium* transformation uses vacuum infiltration in which whole plants are used (Senior, "Uses of Plant Gene Silencing," *Biotechnology and Genetic Engineering Reviews* 15:79-119 (1998), which is hereby incorporated by reference in its entirety).

Yet another method of introduction is fusion of protoplasts with other entities, either minicells, cells, lysosomes, or other fusible lipid-surfaced bodies (Fraley et al., "Liposome-mediated Delivery of Tobacco Mosaic Virus RNA Into Tobacco Protoplasts: A Sensitive Assay for Monitoring Liposome-protoplast Interactions," *Proc. Natl. Acad. Sci. USA* 79:1859-63 (1982), which is hereby incorporated by reference in its entirety). The nucleic acid molecule may also be introduced into the plant cells by electroporation (Fromm et al., "Expression of Genes Transferred into Monocot and Dicot Plant Cells by Electroporation," *Proc. Natl. Acad. Sci. USA* 82:5824 (1985), which is hereby incorporated by reference in its entirety). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the expression cassette. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and regenerate. Other methods of transformation include polyethylene-mediated plant transformation, microinjection, physical abrasives, and laser beams (Senior, "Uses of Plant Gene Silencing," *Biotechnology and Genetic Engineering Reviews* 15:79-119 (1998), which is hereby incorporated by reference in its entirety). The precise method of transformation is not critical to the practice of the present invention. Any method that results in efficient transformation of the host cell of choice is appropriate for practicing the present invention.

After transformation, the transformed plant cells must be regenerated. Plant regeneration from cultured protoplasts is described in Evans et al., *Handbook of Plant Cell Cultures, Vol.* 1, New York, N.Y., MacMillan Publishing Co. (1983); Vasil, ed., *Cell Culture and Somatic Cell Genetics of Plants*, Vol. I (1984) and Vol. III (1986), Orlando, Acad. Press; and Fitch et al., "Somatic Embryogenesis and Plant Regeneration from Immature Zygotic Embryos of Papaya (*Carica papaya* L.)," *Plant Cell Rep.* 9:320 (1990), which are hereby incorporated by reference in their entirety.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts or a petri plate containing explants is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced in the callus tissue. These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is usually reproducible and repeatable.

Preferably, transformed cells are first identified using a selection marker simultaneously introduced into the host cells along with the nucleic acid construct of the present invention. Suitable selection markers include, without limitation, markers encoding for antibiotic resistance, such as the neomycin phosphotransferae II ("nptII") gene which confers kanamycin resistance (Fraley et al., "Expression of Bacterial Genes in Plant Cells," *Proc. Natl. Acad. Sci. USA* 80:4803-4807 (1983), which is hereby incorporated by reference in its entirety), and the genes which confer resistance to gentamycin, G418, hygromycin, streptomycin, spectinomycin, tetracycline, chloramphenicol, and the like. Cells or tissues are grown on a selection medium containing the appropriate antibiotic, whereby generally only those transformants expressing the antibiotic resistance marker continue to grow. Other types of markers are also suitable for inclusion in the expression cassette of the present invention. For example, a gene encoding for herbicide tolerance, such as tolerance to sulfonylurea is useful, or the dhfr gene, which confers resistance to methotrexate (Bourouis et al., *EMBO J.* 2:1099-1104 (1983), which is hereby incorporated by reference in its entirety). Similarly, "reporter genes," which encode for enzymes providing for production of an identifiable compound are suitable. The most widely used reporter gene for gene fusion experiments has been uidA, a gene from *Escherichia coli* that encodes the β-glucuronidase protein, also known as GUS (Jefferson et al., "GUS Fusions: β Glucuronidase as a Sensitive and Versatile Gene Fusion Marker in Higher Plants," *EMBO J.* 6:3901-3907 (1987), which is hereby incorporated by reference in its entirety). Similarly, enzymes providing for production of a compound identifiable by luminescence, such as luciferase, are useful. The selection marker employed will depend on the target species; for certain target species, different antibiotics, herbicide, or biosynthesis selection markers are preferred.

Plant cells and tissues selected by means of an inhibitory agent or other selection marker are then tested for the acquisition of the transgene (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor, N.Y., Cold Spring Harbor Press (1989), which is hereby incorporated by reference in its entirety).

In one embodiment, the transgenic plant is transformed with a bacterial artificial chromosome ("BAC"). A BAC is a cloning vector derived from the naturally occurring F factor of *Escherichia coli*. BACs can accept large inserts of a DNA sequence. In maize, a number of BACs, each containing a large insert of maize genomic DNA, have been assembled into contigs (overlapping contiguous genetic fragments, or "contiguous DNA"). BACs have a propensity for coming together to form contiguous stretches of DNA. A BAC "assembles" to a contig based on sequence alignment, if the BAC is sequenced, or via the alignment of its BAC fingerprint to the fingerprints of other BACs. The assemblies can be found using the Maize Genome Browser, which is publicly available on the internet.

EXAMPLES

The following examples are provided to illustrate embodiments of the present invention but are by no means intended to limit its scope.

Example 1

Detection of QTL and hQTL for Yield-Related Traits and Heterosis

Kernel row number (KRN), kernel count (KC), kernel weight (KW), average kernel weight (AKW), cob weight (CW), cob length (CL), cob diameter (CD), and seedling dry weight (SDW) were measured for above-ground tissues. These traits were selected based on the ability to measure them post-harvest over long periods in the lab and the ability to store samples and re-measure samples with outlying data points. The overall goal of this study was to identify: (1) regions of the genome that regulate yield-related traits and (2) regions of the genome that regulate the amount of heterosis for yield-related traits.

Genetic Stocks

The ISU 291R1SNP Map (N=1,016 markers) was developed using 291 IBM RILs. These RILs were self-pollinated and crossed onto both B73 and Mo17 inbred lines using pollen from the same male (RIL) plant. The seed from a single ear for each cross-type was used in all four biological replications when possible (the use of multiple seed sources was rare).

Seedling Dry Weight Experimental Design

The seedling dry weight experiment was conducted in a greenhouse to reduce environmental effects. Seedlings were grown with 15 hours of light each day. The 291 RILs and their crosses onto B73 and Mo17 were grown in sand benches along with B73, Mo17, B73×Mo17, and Mo17×B73. The design was a randomized complete block design (FIG. **1**), where a RIL and its crosses to B73 and Mo17 (or the parent lines B73, Mo17, and their hybrids) were blocked together, but randomly assigned to a location among the sand benches. The parent lines were sampled more extensively within each replication (50 sets of ~5 seedlings per parent per replication). In each replication, average seedling dry weight at two weeks was recorded based on ~5 seedlings per line.

Due to seed availability, the RILs and their cross-types were divided into two groups for processing (Group A and Group B). For some replications, the planting was distributed over a two-day period. In such cases, half of the rep was planted (sand benches 1-3) on the first day, and half on the second (sand benches 3-6). Harvest was also distributed such that all plants (regardless of planting date) were harvested 2 weeks after planting.

Group A (198 RILs and their crosses to B73 and Mo17), 4 replications (Rep 1, Rep 2, Rep 3, Rep4, and Reps 1B and 2B) were planted and processed in the Fall of the first year and each planting included a single replication. Due to limited daylight in the winter strongly affecting plant growth in the sand benches, the remaining RILs (Group B) were processed in the Fall a year later (Reps 1B and 2B were discarded and regrown in the second season). For RILs or their hybrids failing to germinate in the first year, an alternative seed pack was selected and the RIL and its hybrids were added to the Group B replications in the second year. These instances were not common, however. Because the Group B replications were smaller (~100 RILs and their hybrids), two replications could fit within the greenhouse sand benches in a single growth period (Rep 3B, Rep 4B, Reps 1B-2B redo replications). To estimate the variance from the first year to the second, lines from both Group A (N=95 randomly selected) and Group B (N=all 110) were selected for an additional replication (Rep 5) in the second year.

At harvest, seedlings from a single row/genotype were pooled and stored in a pollination bag and the number of seedlings within the row was recorded. The samples were held in ~60° C. driers housed at the Iowa State University Agronomy Farm for 2-3 days, followed by weight measurements for all tissue within each bag. The per plant dry weight average (g) was calculated based on the total weight of the pooled plants divided by the number of plants in the row.

Adult-Stage Trait Experimental Design

For each of four biological replications, randomization was conducted with restrictions such that inbred and hybrid lines were kept in separate ranges to avoid competition. A triplet of ranges was comprised of 3, 50-row blocks where each block was randomly assigned to contain RIL, B73×RIL, or Mo17×RIL lines. The RIL ranges included 36-37 RILs, 5 B73, 5 Mo17, and 3-4 rows of fill seed/plants (to allow for even distribution of informative lines across the 24 ranges within each replication). Genotypes within the ranges of each triplet were arranged according to the design of the RIL range so that a given RIL and its crosses to B73 and Mo17 were in equivalent positions within neighboring ranges. Positions of the parental lines (B73, Mo17, and F_1 hybrids) were randomly assigned within each set of ranges, maintaining separation of inbred and hybrid lines.

Reps 1-2 and reps 3-4 were planted at the Iowa State University Johnson Farm in Ames, Iowa. Due to excessive flooding, the fourth biological replication was severely damaged and many rows failed to germinate. Thus, only Replications 1-3 were harvested for the QTL study.

Adult-Stage Tissue Sample Processing and Data Collection

The primary ear for each plant was harvested by hand. Harvest was conducted in an order such that within each replication, a given RIL and its hybrids with B73 and Mo17 were harvested, dried, stored, and measured on the same dates. At harvest, two identical harvest tags containing sample information and a unique barcode were affixed to each sample. Ears were then dried for 2-3 days at ~38° C.

Prior to shelling the kernels from the cobs, the number of rows of kernels was counted (KRN) and recorded for each sample. At the shelling stage, kernels from a single ear were stored in a seed envelope and the cob was stored in a sealable, plastic bag, each receiving one of the two identical barcoded labels. Thus, it is possible to relate the kernel and cob data for each plant.

Barcode scanners were used to automatically enter the unique sample identifier (field row and plant-in-row) into MICROSOFT® EXCEL®. Each measurement instrument was equipped to send digital data to a PC through an RS232 cable using WinWedge software (TALtech, Philadelphia, Pa.), allowing for efficient and reliable data entry.

Individual cobs were weighed (CW) using the ATL-822-I digital scale (Acculab, Bradford, Mass.). Cob maximum cob diameter (CD) and length (CL) were measured using a digital caliper (F.V. Fowler, Newton, Mass.). Kernels with mold damage or pest damage were manually filtered from each seed pack. Kernel number (KC) was measured using the Old Mill 850-3 seed counter (International Marketing and Design Co., San Antonio, Tex.). Immediately after, the total kernel weight (KW) for non-filtered kernels was measured using the digital scale (Acculab, Bradford, Mass.). For each sample, average kernel weights (AKW) were calculated by dividing the total weight (g) by the total kernel count (not including the "bad" kernels).

Statistical Analysis

Data were compiled into single spreadsheets for each trait. Quality checks were performed to identify improbable values. Such cases were individually investigated to either confirm the value or correct the error.

LS Means for each genotype were estimated in SAS (company) for the seedling dry weight experiment conducted in the greenhouse using the following model:

proc mixed data=one;

class exp rep sandbench section block crosstype scale;

model y=crosstype scale;

random exp sandbench section(sandbench) block(section sandbench) rep(exp)exp*sandbench exp*section(sandbench)exp*block(section sandbench) sandbench*rep (exp) section*rep(exp sandbench) block*rep(section sandbench exp).

LS Means for each genotype were estimated in SAS (company) using the following model for the field-based traits:

proc mixed data=one;

class rep range col genotype rangeblock dash;

model trait=rep genotype dash/outp=check;

random rangeblock(rep) range(rangeblock rep) col(rangeblock rep) range*col(rangeblock rep)

Mean estimates produced by these models (FIGS. **6**A-U) were used for subsequent QTL mapping. The QTL mapping was conducted using custom R (Version 2.2.1) scripts authored by Dan Nettleton. For each trait and population (RIL, B73×RIL, Mo17×RIL), 11 QTL analyses were conducted (FIGS. **6**A-U).

In addition to mapping each trait per se, QTL for high-parent heterosis ("HPH") and mid-parent heterosis ("MPH") were mapped in the B73×RIL and Mo17×RIL hybrids. HPH and MPH were calculated:

$$HPH=B73\times RIL-\max[B73,RIL]$$

$$HPH=Mo17\times RIL-\max[Mo17,RIL]$$

$$MPH=B73\times RIL-\mathrm{mean}[B73,RIL]$$

$$MPH=Mo17\times RIL-\mathrm{mean}[Mo17,RIL]$$

The resulting HPH and MPH values were then used as input for the QTL analysis. For each significant QTL, the magnitude and direction of effect, percentage variation explained by the QTL, and confidence intervals (1.5 LOD dropdown) were calculated.

Results

Quantitative measures of kernel traits (number of rows, count, weight, average weight), cob traits (length, diameter, and weight), and seedling dry weight were collected for 291 RILs and their hybrids (B73×RIL and Mo17×RIL) in addition to the inbred parents B73, Mo17, and their reciprocal F_1 hybrids. Although hybrids exhibit heterosis for many traits, not all quantitative traits exhibit heterosis (Table 1). Hybrids outperformed their inbred parents for average kernel weight, kernel count per ear, cob weight, cob length, and seedling dry weight. B73 appears dominant for the cob diameter and number of rows of kernels and outperformed the hybrids and Mo17 for both traits.

Multiple QTL were detected within each population and trait (Tables 1-2), some of which overlap across analysis type and trait measured. Using the 1.5 LOD dropdown to determine confidence intervals, ~⅔ of the 85 significant QTL exhibited interval sizes less than 20 cM, but the overall range is from 2.8-149.3 cM. Within traits, the favorable allele for QTL can differ (B73 or Mo17) and the magnitude of effect is variable (13% increase in amount of heterosis for cob weight on Chromosome 1, 6% increase in heterosis for average kernel weight on Chromosome 3).

TABLE 1

QTL Analyses Conducted

No.	Analysis	Comparison	Trait Mapped
1	BxRIL	BxRIL$_{BB}$ vs BXRIL$_{MM}$	BB vs BM
2	RIL	RIL$_{BB}$ vs RIL$_{MM}$	BB vs MM
3	MxRIL	MxRIL$_{BB}$ vs MxRIL$_{MM}$	BM vs MM
4	BxRIL HPH	BxRIL$_{BB}$ vs BxRIL$_{MM}$	High-parent heterosis BB vs BM
5	MxRIL HPH	MxRIL$_{BB}$ vs MxRIL$_{MM}$	High-parent heterosis BM vs MM
6	BxRIL MPH	BxRIL$_{BB}$ vs BxRIL$_{MM}$	Mid-parent heterosis BB vs BM
7	MxRIL MPH	MxRIL$_{BB}$ vs MxRIL$_{MM}$	Mid-parent heterosis BM vs MM
8	BxRIL % HPH	BxRIL$_{BB}$ vs BxRIL$_{MM}$	% High-parent heterosis BB vs BM
9	MxRIL % HPH	MxRIL$_{BB}$ vs MxRIL$_{MM}$	% High-parent heterosis BM vs MM
10	BxRIL % MPH	BxRIL$_{BB}$ vs BxRIL$_{MM}$	% Mid-parent heterosis BB vs BM
11	MxRIL % MPH	MxRIL$_{BB}$ vs MxRIL$_{MM}$	% Mid-parent heterosis BM vs MM

TABLE 2

Significant QTL for All Traits

						Confidence Interval^2					
Trait	Analysis	Sig. Marker	P-value^1	Chr	cM	Lower cM	Upper cM	Length (cM)	Effect Size^3	% Var^4	Action^5
CL	BxRIL	SNP_35511	0.006	1	73.2	71.7	102.9	31.2	−8.37	0.07	BB < BM
CW	M HPH	SNP_98111	0.004	1	78.4	73.2	84	10.8	2.18	0.07	BM > MM
CW	M MPH	SNP_98111	0.012	1	78.4	74.9	215.4	140.5	1.89	0.06	BM > MM
CW	M pHPH	SNP_98111	0.005	1	78.4	73.2	84	10.8	0.13	0.07	BM > MM
CW	M pMPH	SNP_98111	0.006	1	78.4	74.9	84	9.1	0.15	0.07	BM > MM
AKW	RIL	SNP_23951	0.034	1	95.3	79.3	106.4	27.1	−0.02	0.06	BB < MM
KW	BxRIL	SNP_79262	0.02	1	101.6	71.7	104.1	32.4	−13.21	0.05	BB < BM
CL	M pMPH	SNP_19249	0.042	1	175.6	168.2	194.7	26.5	0.05	0.05	BM > MM
KC	M MPH	SNP_9084	0.011	3	87.5	82.5	90.6	8.1	39.62	0.06	BM > MM
KW	M MPH	SNP_9084	0.028	3	87.5	82.9	90.6	7.7	13.19	0.06	BM > MM
KC	MxRIL	SNP_99055	0.024	3	88.2	80.5	93.8	13.3	36.5	0.06	BM > MM
KRN	RIL	SNP_77055	0.007	3	92.9	88.2	229	140.8	0.92	0.07	BB > MM
KRN	MxRIL	SNP_77055	0.001	3	92.9	85	94	9	0.65	0.13	BM > MM
KC	B pHPH	SNP_45551	0.044	3	141.1	135.3	147.2	11.9	-0.1	0.05	BB < BM
AKW	B HPH	SNP_30953	0.004	3	188.7	185	191.4	6.4	-0.02	0.08	BB < BM
AKW	B pHPH	SNP_30953	0.001	3	188.7	185	191.4	6.4	-0.06	0.08	BB < BM
SDW	B HPH	SNP_84678	0.044	3	217.3	80.5	229.8	149.3	-0.01	0.05	BB < BM
SDW	B MPH	SNP_84678	0.01	3	217.3	82.9	229.8	146.9	-0.01	0.06	BB < BM
SDW	B pMPH	SNP_84678	0.016	3	217.3	81.7	229.8	148.1	-0.1	0.06	BB < BM
KC	RIL	SNP_89298_2	0.001	4	16	16	19.5	3.5	62.44	0.08	BB > MM
CW	MxRIL	SNP_32823	0.001	4	41.1	30.1	43.3	13.2	2.48	0.1	BM > MM
CW	RIL	SNP_4623	0.001	4	42.2	30.1	54.5	24.4	3.35	0.11	BB > MM
CD	BxRIL	SNP_90941	0.001	4	54.5	48.2	62.2	14	1.26	0.16	BB > BM
CD	MxRIL	SNP_90941	0.001	4	54.5	48.2	65.6	17.4	0.84	0.12	BM > MM
CD	B HPH	SNP_90941	0.001	4	54.5	48.2	57.4	9.2	1.16	0.14	BB > BM
CD	B pHPH	SNP_90941	0.001	4	54.5	48.2	57.4	9.2	0.04	0.14	BB > BM
CW	BxRIL	SNP_90941	0.001	4	54.5	48.2	62.2	14	2.86	0.09	BB > BM
CW	B HPH	SNP_90941	0.001	4	54.5	48.2	62.2	14	2.5	0.07	BB > BM
CW	B pHPH	SNP_90941	0.003	4	54.5	48.2	62.2	14	0.11	0.08	BB > BM
KRN	MxRIL	SNP_81248	0.001	4	54.5	30.1	62.2	32.1	0.51	0.09	BM > MM
CD	RIL	SNP_82913	0.001	4	57.4	48.2	65.6	17.4	1.64	0.16	BB > MM
KRN	RIL	SNP_82913	0.001	4	57.4	48.2	65.6	17.4	1.32	0.15	BB > MM
KRN	M HPH	SNP_82913	0.001	4	57.4	54.7	65.6	10.9	−0.87	0.13	BM < MM
KRN	M pHPH	SNP_82913	0.001	4	57.4	54.7	65.6	10.9	−0.06	0.13	BM < MM
CD	M HPH	SNP_93907	0.006	4	62.2	8.1	100.3	92.2	−0.79	0.07	BM < MM
CD	M pHPH	SNP_93907	0.014	4	62.2	8.1	100.3	92.2	−0.03	0.06	BM < MM
KW	RIL	SNP_93907	0.021	4	62.2	16	100.3	84.3	13.82	0.06	BB > MM
KRN	BxRIL	SNP_90380	0.001	4	65.6	48.2	67.5	19.3	0.75	0.11	BB > BM
KRN	B HPH	SNP_90380	0.001	4	65.6	48.2	67.5	19.3	0.67	0.1	BB > BM
KRN	B pHPH	SNP_90380	0.002	4	65.6	48.2	67.5	19.3	0.04	0.1	BB > BM
CL	RIL	SNP_49724	0.022	5	44.2	42.9	55.1	12.2	−10.16	0.06	BB < MM
KC	MxRIL	SNP_51496	0.011	5	73.8	66.8	85.5	18.7	39.15	0.07	BM > MM
KRN	RIL	SNP_11948	0.001	5	73.8	70.8	76.5	5.7	1.03	0.09	BB > MM
SDW	MxRIL	SNP_18689	0.012	5	73.8	69.1	91.2	22.1	0.01	0.06	BM > MM
SDW	M HPH	SNP_18689	0.032	5	73.8	69.1	76.5	7.4	0.01	0.06	BM > MM

TABLE 2-continued

Significant QTL for All Traits

						Confidence Interval[2]					
Trait	Analysis	Sig. Marker	P-value[1]	Chr	cM	Lower cM	Upper cM	Length (cM)	Effect Size[3]	% Var[4]	Action[5]
SDW	M MPH	SNP_18689	0.029	5	73.8	69.1	75.9	6.8	0.01	0.06	BM > MM
SDW	M pHPH	SNP_18689	0.046	5	73.8	69.1	76.5	7.4	0.08	0.05	BM > MM
KRN	BxRIL	SNP_61221	0.012	5	75.7	70.8	76.6	5.8	0.55	0.06	BB > BM
KRN	MxRIL	SNP_61221	0.006	5	75.7	70.8	98.6	27.8	0.46	0.07	BM > MM
CD	MxRIL	SNP_105143	0.005	5	75.9	61.5	76.6	15.1	0.63	0.07	BM > MM
KW	MxRIL	SNP_84372	0.001	5	81.6	72.2	85.5	13.3	15.19	0.08	BM > MM
KW	M HPH	SNP_84372	0.026	5	81.6	70.8	113.8	43	13.2	0.06	BM > MM
KW	M MPH	SNP_84372	0.009	5	81.6	70.8	105.7	34.9	13.97	0.06	BM > MM
CW	MxRIL	SNP_27764	0.01	5	113.8	66.8	126	59.2	2.04	0.07	BM > MM
CW	M MPH	SNP_95039	0.018	5	113.8	105.7	126	20.3	1.89	0.06	BM > MM
CW	BxRIL	SNP_75795	0.003	6	114.2	102.3	116.4	14.1	−2.58	0.07	BB < BM
CW	B HPH	SNP_75795	0.018	6	114.2	102.3	119.6	17.3	−2.36	0.06	BB < BM
CW	B pHPH	SNP_75795	0.021	6	114.2	102.3	119.6	17.3	−0.1	0.06	BB < BM
KRN	RIL	SNP_70805	0.003	7	34.5	28.6	36	7.4	−0.95	0.08	BB < MM
CD	RIL	SNP_43846	0.049	7	42.2	22	101.2	79.2	−0.97	0.05	BB < MM
CD	BxRIL	SNP_98032	0.033	7	43.6	22	101.2	79.2	−0.77	0.05	BB < BM
KC	RIL	SNP_63437	0.043	7	65.5	59.4	71.6	12.2	−50.81	0.05	BB < MM
KRN	BxRIL	SNP_94161	0.026	7	78.3	65.5	82.1	16.6	−0.54	0.06	BB < BM
KRN	B HPH	SNP_94161	0.027	7	78.3	65.5	82.1	16.6	−0.53	0.06	BB < BM
KRN	B pHPH	SNP_94161	0.022	7	78.3	65.5	82.1	16.6	−0.03	0.06	BB < BM
CW	B HPH	SNP_34738	0.037	7	85.8	82.1	88.5	6.4	−2.18	0.05	BB < BM
CW	B pHPH	SNP_34738	0.044	7	85.8	82.1	88.5	6.4	−0.09	0.05	BB < BM
CD	BxRIL	SNP_88270	0.02	8	43.6	36.7	46.7	10	−0.77	0.06	BB < BM
CD	B HPH	SNP_88270	0.008	8	43.6	36.7	46.7	10	−0.77	0.06	BB < BM
CD	B MPH	SNP_88270	0.01	8	43.6	36.7	46.7	10	−0.58	0.06	BB < BM
CD	B pHPH	SNP_88270	0.009	8	43.6	36.7	46.7	10	−0.03	0.06	BB < BM
CD	B pMPH	SNP_88270	0.018	8	43.6	36.7	46.7	10	−0.02	0.05	BB < BM
KRN	MxRIL	SNP_2880	0.022	8	80.9	78.7	89.8	11.1	0.44	0.06	BM > MM
KRN	M MPH	SNP_36300	0.015	10	1.5	0	2.8	2.8	−0.32	0.06	BM < MM
KRN	M pMPH	SNP_36300	0.013	10	1.5	0	2.8	2.8	−0.03	0.06	BM < MM
CD	BxRIL	SNP_77712	0.001	10	53.4	50.2	58.1	7.9	−1	0.08	BB < BM
CD	B HPH	SNP_77712	0.002	10	53.4	50.2	58.1	7.9	−0.94	0.08	BB < BM
CD	B MPH	SNP_77712	0.002	10	53.4	50.2	58.1	7.9	−0.69	0.07	BB < BM
CD	B pHPH	SNP_77712	0.001	10	53.4	50.2	58.1	7.9	−0.03	0.08	BB < BM
CD	B pHPH	SNP_77712	0.004	10	53.4	50.2	58.1	7.9	−0.03	0.06	BB < BM
CW	BxRIL	SNP_77712	0.003	10	53.4	50.2	59.5	9.3	−2.59	0.07	BB < BM
CW	B HPH	SNP_77712	0.003	10	53.4	50.2	65.5	15.3	−2.46	0.06	BB < BM
CW	B MPH	SNP_77712	0.039	10	53.4	50.2	71.6	21.4	−2.01	0.05	BB < BM
CW	B pHPH	SNP_77712	0.007	10	53.4	50.2	65.5	15.3	−0.1	0.07	BB < BM

[1] Genome-wise error rate P-Value;

[2] Confidence interval determined by 1.5 LOD drop-down from significant peak

[3] B73xRIL$_{BB}$ − B73xRIL$_{MM}$ (B73xRIL); Mo17xRIL$_{BB}$ − Mo17xRIL$_{MM}$ (Mo17xRIL), RIL$_{BB}$ − RIL$_{MM}$ (RIL)

[4] Percent variation explained by the QTL

[5] Direction of effect for significant QTL

QTL for amount of heterosis were detected where heterozygous lines exhibited more heterosis than the homozygotes (B73×RIL HPH for AKW, SDW, CW, KRN, and CD; Mo17×RIL HPH for CW, SDW). QTL were also detected, however, with homozygous loci favorable over heterozygous loci. Variation of effect size and favorable allele combination suggest that not one single inbred (B73 or Mo17) contributes "more" to heterosis and that heterozygosity per se is not sufficient to explain improved performance of hybrids over inbreds for these particular traits.

Correlation between traits was calculated (Table 3). High correlation between some traits was expected. For example, the total kernel weight per ear would be expected to increase with the total number of kernels on the ear (correlation=0.94). Correlations between seedling dry weight and all other traits are generally low, but might be due to different environments (greenhouse vs. field). However, some correlation is observed for seedling dry weight with cob length and kernel weights.

TABLE 3

Pair-wise Trait Correlation of LS Means for Each Genotype

	CW	CD	CL	KRN	KW	KC	AKW	SDW
CW	—							
CD	0.78	—						
CL	0.66	0.25	—					
KRN	0.46	0.73	−0.17	—				
KW	0.24	0.53	0.8	0.24	—			
KC	0.84	0.64	0.69	0.46	0.94	—		
AKW	0.45	0.13	0.65	−0.28	0.65	0.39	—	
SDW	0.35	0.08	0.5	−0.09	0.52	0.42	0.45	—

QTL controlling an increase in the trait value and/or in the amount of heterosis observed for the trait have been selected for fine-mapping experiments with the ultimate goal of cloning the gene(s) responsible for the increase in trait value and/or amount of heterosis.

Example 2

Detection of KRN QTL in the Nested Association Mapping (NAM) Population of Maize

Genetic Stocks

The Maize Nested Association Mapping ("NAM") population was formed by crossing 25 diverse lines to the inbred B73, and then ~200 RILs were created from each of the 25 families. The NAM RIL genetic stocks are publicly available upon request to the Maize Genetics Cooperation Stock Center. During the summer nursery season of two different years, approximately ⅔ of the NAM RILs were planted in 5 plant rows in Ames, Iowa.

Data Collection

All plants were self-pollinated. A photograph was taken of each of the mature ears. KRN data were obtained by manually counting the number of rows on each ear that are visible in the photographs and by subsequently correcting for the rows that are hidden on the far side of each ear. A quality score ("QS") was assigned for each KRN count. The QS ranged from 0 to 5, indicating a confidence level of KRN count that could be collected from the photograph. Four terms were taken into consideration when assigning QS: whether the ear was developed, whether there were missing kernels in any rows, whether there were twisted kernel rows, and whether any partial rows were visible in the photo.

Data were entered into spreadsheets. Quality checks were performed to identify improbable values. Such cases were individually investigated to either confirm the value or correct the error.

Statistical Analysis

Raw KRN counts (X) were transformed using the formula 2x+2 which a pilot study indicated did the best job of converting KRN counts from photograph to numbers that would match counts obtained by determined KRNs directly from ears. These corrected KRN values were used for QTL mapping via each of two methods. The first method ("wmean") used weighted means, in which the KRN count is weighted by the QS to calculate the mean value of a specific RIL. The other method ("trim") makes use of a trimmed weighted mean, in which values with QS</=2 are removed prior to QTL analysis.

Mean estimates of KRN for each NAM RIL were used for subsequent QTL mapping. The QTL mapping was conducted using package R/qtl (Version 1.16-4) and custom scripts were developed to format and visualize the results. A separate QTL mapping analysis was conducted for each of the analyzed NAM populations. Mapping was conducted using the standard interval method (EM algorithm). The significance threshold was determined using 1,000 permutation tests. The confidence intervals were calculated based on the 1.5 LOD dropdown values. Results are set forth in Table 4.

TABLE 4

QTL for KRN

Population (B73x)	Method	Chr	Sig. Pos.	Sig. Marker	Locus Name	Marker Name	LOD	Threshold	Confidence Interval	C.I. Length
CML333	wmean	1	116.2	L00401	L00401	PZA01216.1	3.96	3.18	94.9-124.2	29.3
CML333	trim	1	116.2	L004011	L00401	PZA01216.1	3.86	2.94	109.9-124.2	14.3
I114H	wmean	1	28	c 1.loc28	L00454	PZA01497.1	3.41	3.02	20.1-37.8	17.7
I114H	wmean	2	69.4	L01176	L01176	PZB00183.4	4.54	3.02	64.2-71.3	7.1
I114H	trim	2	70	c 2.loc70	L00644	PZA02450.1	4.52	3.1	64.2-71.3	7.1
Ky21	wmean	2	66	c 2.loc66	L00538	PZA01993.7	3.47	3.04	54.9-103.7	48.8
P39	wmean	2	54.9	L01157	L01157	PZA03142.5	3.41	3.09	52-85.5	33.5
CML322	wmean	3	55.5	L00033	L00951	zb21.1	3.12	3.07	50.2-68.9	18.7
CML322	trim	3	55.5	L000331	L00951	zb21.1	3.15	3.1	38.3-68.9	30.6
Ms71	wmean	3	54.3	L00198c	L00198c	PZA00210.1/9	5.2	2.96	50.2-57.6	7.4
Ms71	trim	3	54.3	L00198c1	L00198c	PZA00210.1/9	5.18	2.99	50.2-57.6	7.4
P39	wmean	3	52	c 3.loc52	L00641	PZA02427.1	3.29	3.09	33.7-90	56.3
CML103	wmean	4	119.8	L01138	L01138	PZA02585.2	4.36	2.96	111.5-135.6	24.1
CML103	trim	4	119.8	L011381	L01138	PZA02585.2	3.48	2.92	110.4-141.1	30.7
CML322	wmean	4	126	c 4.loc126	L00067	PHM2100.21	3.43	3.07	111.3-135.6	24.3
CML322	trim	4	126	c 4.loc1261	L00067	PHM2100.21	4.47	3.1	116.1-129.3	13.2
CML228	wmean	4	115.2	L00280	L00280	PZA00521.3	3.51	3.06	107.4-136.6	29.2
CML333	trim	4	119.6	L00133	L00133	PHM5599.20	4.41	2.94	115.2-126.9	11.7
Ki11	wmean	4	106	c 4.loc106	L01014	PZA00193.2	3.41	3.02	85.2-115.2	30
Ms71	wmean	4	55.2	L01028	L01028	PZA00445.22	4.61	2.96	40.4-69.8	29.4
Ms71	trim	4	55.2	L010281	L01028	PZA00445.22	4.6	2.99	43.9-76.2	32.3
Oh43	wmean	4	118.4	L00576	L00576	PZA02151.3	6.96	3.05	81.9-124.5	42.6
Oh43	trim	4	118.4	L005761	L00576	PZA02151.3	7.2	3.07	81.9-124.5	42.6
P39	wmean	4	52	c 4.loc52	L00042	PHM15427.11	3.36	3.09	33.9-135.6	101.7
P39	trim	4	52	c 4.loc521	L00042	PHM15427.11	3.51	3.11	33.9-135.6	101.7
Tx303	trim	4	114	c 4.loc114	L00280	PZA00521.3	3.72	2.96	60.6-124.5	63.9
B97	wmean	5	60.6	L00589	L00589	PZA02207.1	4.04	3.09	47-78.4	31.4
B97	trim	5	53.9	L00134	L00134	PHM565.31	3.65	3.08	47-78.4	31.4
I114H	wmean	5	47	c 5.loc47	L00835	PZA03578.1	5.07	3.02	41.5-80.7	39.2
I114H	trim	5	47	c 5.loc471	L00835	PZA03578.1	5.02	3.1	41.5-81.7	40.2
Oh43	wmean	5	83.4	L00221	L00221	PZA00300.14	4.89	3.05	81.7-87.2	5.5
Oh43	trim	5	83.4	L002211	L00221	PZA00300.14	4.76	3.07	78.4-87.2	8.8
Tx303	wmean	5	73	c 5.loc73	L00171	PZA00067.10	4.03	3.09	57.3-87.2	29.9
Tx303	trim	5	57.6	L00110	L00461	PZA01563.1	3.5	2.96	50.8-87.2	36.4
CML333	wmean	10	51	c10.loc51	L01041	PZA00647.9	6.44	3.18	44.8-61.6	16.8
CML333	trim	10	50	c10.loc50	L00367	PZA01005.1	5.2	2.94	44.8-75.4	30.6

Notes:
wmean, weighted mean of the KRN count;
trim, trimmed mean of the KRN count.

Although the invention has been described in detail for the purposes of illustration, it is understood that such detail is solely for that purpose, and variations can be made therein by those skilled in the art without departing from the spirit and scope of the invention which is defined by the following claims.

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cgcgattcgg tcaccgaaca aacaaacaaa caaacaacaa acccctccgc ggcactcatc     60

wtcagtccaa aacgacactt ccaccccggc aacagtcaag ctcactttcc gcgagcagga    120

g                                                                    121


<210> SEQ ID NO 35
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_34738
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<400> SEQUENCE: 35

attgtttttt cattgcgaac actctagtag gccatttatc tacggttttt tcactatatt   60

yattaagata ttatgagatt tcacattgcc ttgtaaagac aaatctctag ccatgtttgg   120

t   121

<210> SEQ ID NO 36
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_88270

<400> SEQUENCE: 36

attcacgacc catttaatca ggaaccacgc acaatgtgta tatcataaat agaaatcccc   60

rattgcagat aacaattgtg gaatagaaac gtaatacaaa aggtagattt tagaaaggac   120

a   121

<210> SEQ ID NO 37
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_2880

<400> SEQUENCE: 37

cgttcaagtg agatattcaa ttgttcagat attcaaattc tttgaaaaac tcagcacaaa   60

yattcaaatg ttcagatatt caaattcttc gaaaatgttc agactttaga caaaaagtaa   120

c   121

<210> SEQ ID NO 38
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_36300

<400> SEQUENCE: 38

ccacctccga agatactgta gattcctatg atcatttggc tgcattgttc cggccacctg   60

wcgccgtctc gccggttgga gcagcaggac caaattccct tgcgtggctc ctgctctttg   120

c   121

<210> SEQ ID NO 39
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_77712

<400> SEQUENCE: 39

agaaatgttc attgtcatat tgggcatcca tccacaggca cagttcagcg ggattttaag   60

kctgagttca tcgctttttc aacccgtccg aagctaccaa catcagagcg gtaggggagg   120

c   121

<210> SEQ ID NO 40
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_35511 forward primer

<400> SEQUENCE: 40

acgttggatg gtctactagt aagttctctc 30

<210> SEQ ID NO 41
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_98111 forward primer

<400> SEQUENCE: 41

acgttggatg cgtaggcaga gactcaaaag 30

<210> SEQ ID NO 42
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_23951 forward primer

<400> SEQUENCE: 42

acgttggatg caacaggaga ttgttgtggg 30

<210> SEQ ID NO 43
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_79262 forward primer

<400> SEQUENCE: 43

acgttggatg caaggatcat acgtcgcaac 30

<210> SEQ ID NO 44
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_19249 forward primer

<400> SEQUENCE: 44

acgttggatg gccttgatac attgttacag 30

<210> SEQ ID NO 45
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_0984 forward primer

<400> SEQUENCE: 45

acgttggatg actcgacaca tgtgtgcaac 30

<210> SEQ ID NO 46
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_99055 forward primer

<400> SEQUENCE: 46

acgttggatg tatcgaccct attacgtgcc 30

<210> SEQ ID NO 47

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<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_77055 forward primer

<400> SEQUENCE: 47

acgttggatg ttgtgaaatg cgatccagcg                                      30


<210> SEQ ID NO 48
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_45551 forward primer

<400> SEQUENCE: 48

acgttggatg acatacctca atcatcggtc                                      30


<210> SEQ ID NO 49
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_30953 forward primer

<400> SEQUENCE: 49

acgttggatg catggctgat ggatcaaaag                                      30


<210> SEQ ID NO 50
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_84678 forward primer

<400> SEQUENCE: 50

acgttggatg gcgatggagc gatgtataac                                      30


<210> SEQ ID NO 51
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_89298_2 forward primer

<400> SEQUENCE: 51

acgttggatg tgttgaaagg atgccacagg                                      30


<210> SEQ ID NO 52
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_32823 forward primer

<400> SEQUENCE: 52

acgttggatg tctgcaaagt gagtaattcg                                      30


<210> SEQ ID NO 53
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_4623 forward primer

<400> SEQUENCE: 53
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acgttggatg ttgcatgagg agctcatacg                                        30


<210> SEQ ID NO 54
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_90941 forward primer

<400> SEQUENCE: 54

acgttggatg attattccag cagcgatgtg                                        30


<210> SEQ ID NO 55
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_81248 forward primer

<400> SEQUENCE: 55

acgttggatg gtgatgtgta tctcttaggc                                        30


<210> SEQ ID NO 56
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_82913 forward primer

<400> SEQUENCE: 56

acgttggatg gttttggccc caatatacgc                                        30


<210> SEQ ID NO 57
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_93907 forward primer

<400> SEQUENCE: 57

acgttggatg gcagcactga ctttttttccg                                        30


<210> SEQ ID NO 58
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_90380 forward primer

<400> SEQUENCE: 58

acgttggatg cacaaacttt tagccgcgtg                                        30


<210> SEQ ID NO 59
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_49724 forward primer

<400> SEQUENCE: 59

acgttggatg tgagttattc tcaggctgcg                                        30


<210> SEQ ID NO 60
<211> LENGTH: 30
<212> TYPE: DNA
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<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_51496 forward primer

<400> SEQUENCE: 60

acgttggatg aacaaatggt acaccgggac                                        30


<210> SEQ ID NO 61
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_11948 forward primer

<400> SEQUENCE: 61

acgttggatg tgctacatcc ttgagctgac                                        30


<210> SEQ ID NO 62
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_18689 forward primer

<400> SEQUENCE: 62

acgttggatg atagcaaaga ccgcctttcc                                        30


<210> SEQ ID NO 63
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_61221 forward primer

<400> SEQUENCE: 63

acgttggatg cgacttaaat ttcgtttccc c                                      31


<210> SEQ ID NO 64
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_105143 forward primer

<400> SEQUENCE: 64

acgttggatg ccgttaagaa tcacgagatg                                        30


<210> SEQ ID NO 65
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_84372 forward primer

<400> SEQUENCE: 65

acgttggatg gattaagaga agtgtttggg c                                      31


<210> SEQ ID NO 66
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_27764 forward primer

<400> SEQUENCE: 66

acgttggatg ggagaacaag ttgaacatct g                                      31
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<210> SEQ ID NO 67
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_95039 forward primer

<400> SEQUENCE: 67

acgttggatg gccgggataa aaattctcca 30

<210> SEQ ID NO 68
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_75795 forward primer

<400> SEQUENCE: 68

acgttggatg cttgttgaag agaacgctgg 30

<210> SEQ ID NO 69
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_70805 forward primer

<400> SEQUENCE: 69

acgttggatg ccaaccgagt aacctcatac 30

<210> SEQ ID NO 70
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_43846 forward primer

<400> SEQUENCE: 70

acgttggatg agtatatata ggaggagtgc 30

<210> SEQ ID NO 71
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_98032 forward primer

<400> SEQUENCE: 71

acgttggatg tgctatatgg tgtagcgtcc 30

<210> SEQ ID NO 72
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_63437 forward primer

<400> SEQUENCE: 72

acgttggatg taccatgcag cctcttgttg 30

<210> SEQ ID NO 73
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:

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<223> OTHER INFORMATION: SNP_94161 forward primer

<400> SEQUENCE: 73

acgttggatg aaacaacaaa cccctccgc                                          29


<210> SEQ ID NO 74
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_34738 forward primer

<400> SEQUENCE: 74

acgttggatg agtaggccat ttatctacgg                                         30


<210> SEQ ID NO 75
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_88270 forward primer

<400> SEQUENCE: 75

acgttggatg atcaggaacc acgcacaatg                                         30


<210> SEQ ID NO 76
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_2880 forward primer

<400> SEQUENCE: 76

acgttggatg caaattcttt gaaaaactca g                                       31


<210> SEQ ID NO 77
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_36300 forward primer

<400> SEQUENCE: 77

acgttggatg catttggctg cattgttccg                                         30


<210> SEQ ID NO 78
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_77712 forward primer

<400> SEQUENCE: 78

acgttggatg cttcggacgg gttgaaaaag                                         30


<210> SEQ ID NO 79
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_35511 reverse primer

<400> SEQUENCE: 79

acgttggatg gcgtctgtat acctatgtat g                                       31
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<210> SEQ ID NO 80
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_98111 reverse primer

<400> SEQUENCE: 80

acgttggatg taccttcgtc gatcaccttg                                 30


<210> SEQ ID NO 81
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_23951 reverse primer

<400> SEQUENCE: 81

acgttggatg tgaagcctac attcagagcc                                 30


<210> SEQ ID NO 82
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_79262 reverse primer

<400> SEQUENCE: 82

acgttggatg gtcaagacct cacgcatatc                                 30


<210> SEQ ID NO 83
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_19249 reverse primer

<400> SEQUENCE: 83

acgttggatg taaaagtggc cgtgtgactg                                 30


<210> SEQ ID NO 84
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_0984 reverse primer

<400> SEQUENCE: 84

acgttggatg tgtaagcatc cctctatcgg                                 30


<210> SEQ ID NO 85
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_99055 reverse primer

<400> SEQUENCE: 85

acgttggatg gtgcgtcctt gtttcttttc                                 30


<210> SEQ ID NO 86
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_77055 reverse primer
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<400> SEQUENCE: 86

acgttggatg tcagagtttt acggtgtggg 30

<210> SEQ ID NO 87
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_45551 reverse primer

<400> SEQUENCE: 87

acgttggatg actggtcttc agctcattag 30

<210> SEQ ID NO 88
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_30953 reverse primer

<400> SEQUENCE: 88

acgttggatg gatatctaga tcgaagcggg 30

<210> SEQ ID NO 89
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_84678 reverse primer

<400> SEQUENCE: 89

acgttggatg ttgctactga tattggtccc 30

<210> SEQ ID NO 90
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_89298_2 reverse primer

<400> SEQUENCE: 90

acgttggatg tgacattttg cgcacatggg 30

<210> SEQ ID NO 91
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_32823 reverse primer

<400> SEQUENCE: 91

acgttggatg gcgaatactc tggttatgcc 30

<210> SEQ ID NO 92
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_4623 reverse primer

<400> SEQUENCE: 92

acgttggatg gcatgcacta agaacatgaa g 31

<210> SEQ ID NO 93
<211> LENGTH: 30

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<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_90941 reverse primer

<400> SEQUENCE: 93

acgttggatg tcagaccatc ctttagcgtg                                        30


<210> SEQ ID NO 94
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_81248 reverse primer

<400> SEQUENCE: 94

acgttggatg gcacaagccc agtaaatcag                                        30


<210> SEQ ID NO 95
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_82913 reverse primer

<400> SEQUENCE: 95

acgttggatg cggatgtgta tcaatccgtg                                        30


<210> SEQ ID NO 96
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_93907 reverse primer

<400> SEQUENCE: 96

acgttggatg ctgcttcatg tgtagctttc                                        30


<210> SEQ ID NO 97
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_90380 reverse primer

<400> SEQUENCE: 97

acgttggatg tcgcggatcg taaattagtg                                        30


<210> SEQ ID NO 98
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_49724 reverse primer

<400> SEQUENCE: 98

acgttggatg tgtgggtgct tcgttttgag                                        30


<210> SEQ ID NO 99
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_51496 reverse primer

<400> SEQUENCE: 99
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<210> SEQ ID NO 100
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_11948 reverse primer

<400> SEQUENCE: 100

acgttggatg actgaattga gtttgggacg                                        30


<210> SEQ ID NO 101
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_18689 reverse primer

<400> SEQUENCE: 101

acgttggatg tcgctttgga ttttcactgg                                        30


<210> SEQ ID NO 102
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_61221 reverse primer

<400> SEQUENCE: 102

acgttggatg ctgcagtagc ttagtccatc                                        30


<210> SEQ ID NO 103
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_105143 reverse primer

<400> SEQUENCE: 103

acgttggatg gagacctcac ttatccatgt                                        30


<210> SEQ ID NO 104
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_84372 reverse primer

<400> SEQUENCE: 104

acgttggatg taacgaagct ttgcccactg                                        30


<210> SEQ ID NO 105
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_27764 reverse primer

<400> SEQUENCE: 105

acgttggatg gaagtacatg gtaaaggacg                                        30


<210> SEQ ID NO 106
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
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<220> FEATURE:
<223> OTHER INFORMATION: SNP_95039 reverse primer

<400> SEQUENCE: 106

acgttggatg tggcataggt ctaatccctc                                      30


<210> SEQ ID NO 107
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_75795 reverse primer

<400> SEQUENCE: 107

acgttggatg acgataagaa tggtgccgtg                                      30


<210> SEQ ID NO 108
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_70805 reverse primer

<400> SEQUENCE: 108

acgttggatg agtagggacg gtgtaattgg                                      30


<210> SEQ ID NO 109
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_43846 reverse primer

<400> SEQUENCE: 109

acgttggatg ggactgtagt gtgcgtactg                                      30


<210> SEQ ID NO 110
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_98032 reverse primer

<400> SEQUENCE: 110

acgttggatg gtacttgatg actgttgacg                                      30


<210> SEQ ID NO 111
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_63437 reverse primer

<400> SEQUENCE: 111

acgttggatg cgcacaggta gccatctata                                      30


<210> SEQ ID NO 112
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_94161 reverse primer

<400> SEQUENCE: 112

acgttggatg aagtgagctt gactgttgcc                                      30
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<210> SEQ ID NO 113
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_34738 reverse primer

<400> SEQUENCE: 113

acgttggatg gagatttgtc tttacaaggc 30

<210> SEQ ID NO 114
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_88270 reverse primer

<400> SEQUENCE: 114

acgttggatg gtattacgtt tctattccac 30

<210> SEQ ID NO 115
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_2880 reverse primer

<400> SEQUENCE: 115

acgttggatg gttacttttt gtctaaagtc 30

<210> SEQ ID NO 116
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_36300 reverse primer

<400> SEQUENCE: 116

acgttggatg aagggaattt ggtcctgctg 30

<210> SEQ ID NO 117
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: SNP_77712 reverse primer

<400> SEQUENCE: 117

acgttggatg gtcatattgg gcatccatcc 30

<210> SEQ ID NO 118
<211> LENGTH: 160
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA01216.1

<400> SEQUENCE: 118

ggtatgttca ttttgctata tttatggtga accgttgaat gtgactggga taatgatgty 60

agaaaaggca ttgaaacttg tcatcggtgc ccatccagtt aatttctacg accgtaaaaa 120

aataagccac tgcaactgtt ttacaagaag tattcatgtg 160

<210> SEQ ID NO 119
<211> LENGTH: 225

<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA01497.1

<400> SEQUENCE: 119

atacgtatac cggagatgaa aggagacgga ggcagtgaag aaatatcctt ttttttcttc 60

tcrtttttca cgaggatgcs gtgcactgct cccagaatgc tgtgtccaat ttacaaacgc 120

acaggtggca catgaactag cagagtagct ytmtcttgaa aggaaactgt atttggggtc 180

gatgaaccct ctggtgttat tcttcagack ggtaaacgat ktaac 225

<210> SEQ ID NO 120
<211> LENGTH: 385
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZB00183.4

<400> SEQUENCE: 120

gctccagttc atcagscggt gsgactgcgg atgcctaccc aratagctcc tactagagac 60

gtcagcttcg tcggcrgcga aggcgtccga atggcccgac gccgcaggag gcgaccagac 120

cgggaccacg gcgccctctc tgccggtcca gctgctcgaa gcctccgacg cygacggagc 180

aagcagagcw tctcgcctgt ggttccgasg ctgctggaag rcgtcgtgct ggcgagcgcc 240

rttgttggtt ctacgcgcag ctggcggggc ttcggctckk gggtggagat ggagatgcgc 300

gtggaacgga acctgcgccc tggtgtcctc ctcctcgctg ttcgctactr ctagatcggc 360

ggagacctct gttccagctc tgttc 385

<210> SEQ ID NO 121
<211> LENGTH: 247
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA02450.1

<400> SEQUENCE: 121

gacctactca tcattttcct gaacattttc cagaacggta acttgtacat tatgtctact 60

gctgccattt tttaatgagc ccaggtatct gagaaaagtg aaatgtcaaa tatcaggtca 120

aggcaaggag aaagaaaagg tggagaaact gcatatkttt caaaccataa aggtgagaga 180

gctaacgama ggttcattac tgacctcrac accrttaggc cctattttgt tgcgggatat 240

gaacttc 247

<210> SEQ ID NO 122
<211> LENGTH: 151
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA01993.7

<400> SEQUENCE: 122

ttgcaatctc atatcttgaa tctcacacca agcataataa ttcacattga aagygtctga 60

cctatcctct agcagttgtc gacaaattts tccagttcat gtacagtaga aaccgatgcg 120

ttgcagtytc agaacatctt cacttcagat a 151

<210> SEQ ID NO 123
<211> LENGTH: 349
<212> TYPE: DNA

<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA03142.5

<400> SEQUENCE: 123

agtgcccgcg cttgatgtcc gggcgcaggt agttggtcca ccgcagccgg cagctcttrc 60

cgcaccggtt cagccctgca tgcatgcccr crrgtcgcty aagaaatgac gagcacgagg 120

craacaacta ggtcacgcat gcagcaccag gmrgccgggc ygggctcgac cgaggaacag 180

agcacacgta cgtacccgcg agcttgggga gcatgcgcca atttccggcr ccgttggcct 240

ggacgtagtc gacgagcagc ttgtcctcct ccagcgccca ctgtcccttc ttgatcccmt 300

tgctgtsgca gcacggastt ctycccatgg cgrtcggtcg ctctccgtc 349

<210> SEQ ID NO 124
<211> LENGTH: 189
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: zb21.1
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (169)..(172)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 124

ctacaaagtg accaaccatt tcatggaatt gcttcaaacc cgagagcggc aagataatag 60

acgaacgatc agctccagcc acctgtaagt acaatcacaa ayrgtaagag caatggatca 120

ctygtggagg cttgtgttta caaataatrg ccaacaacak gttacctcnn nnatcctcaa 180

ataatggcc 189

<210> SEQ ID NO 125
<211> LENGTH: 303
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA00210.1

<400> SEQUENCE: 125

tcccttagga agtatctaca tcagcaggag cctcactcag ttcccctcaa cmtagtgctg 60

aaattagctc tagatatygc tcgyggaatg agctacctac actcccaggg tatactccat 120

agrgacctga aatcagagaa crtacttctg ggagaagata tgtcagtcaa agtygcagat 180

ttcgggattt catgcttgga atcacagtgt ggaagtggca aggggtttac aggaacctac 240

aggtggatgg ctccrgagat gatcaaagag gaacatcata ctaggaaagt ggacgtgtac 300

agc 303

<210> SEQ ID NO 126
<211> LENGTH: 250
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA02427.1

<400> SEQUENCE: 126

cmatggtaca cgtaacccgg accmgtggtg acgtcgaagg ggamgcggst ctcctccggc 60

gacgcggcgt ctgtgagcgg cttgaagcgc acgaggatcc kggttaccgc gctgggccgc 120

accttgaaga cgttcttcca gccgcgctcc tgccgcggca cgacgtgcct ccgcsmgccg 180

gccaggtggc ggtcgacccc gcacgcgcgc gcgtcgttcc ggcgcttcat gcagtccctg 240

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aastcgtcca                                                          250


<210> SEQ ID NO 127
<211> LENGTH: 246
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA02585.2

<400> SEQUENCE: 127

cttcctgatc ttcttggcrg tcgtgcaatt ccccatgctg ttctggctcg gcaacatatg     60

tggctgacct ttgatcctat tggtcgggcc acagacctgt ttcttcttct tcttcagaat    120

aggcatgtgc tacttctggc ttgstgatga awcttaggtt tatcgtggag atggtacaga    180

actattagct atagatatct gggcaatcga aaactgtttt tgtttctgtt agctatakag    240

gcgaaa                                                              246


<210> SEQ ID NO 128
<211> LENGTH: 770
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PHM2100.21
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (67)..(67)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (83)..(83)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (87)..(87)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (92)..(93)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (95)..(100)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (107)..(107)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (284)..(284)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (302)..(302)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (308)..(308)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 128

gaaggggggg gcccggagna aattwctyyc cssssgggwa wwwawcwwwa warararadhhh     60

hmmmvrnvsg rrrrrdrrmh mhnvbsndrd dnnbnnnnnn hwwaddnbss ccttttttgbb    120

tkgscywwty ymccyhaawc agawwtwmcy skhhbgryyy dwyyhwamaw wtttttwaaa    180
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atkagktacg awarrggyyy waadawkgcd twaccmgtyt waaaaasgtc mgaaycmytc    240

cmggccyttb ggaammmckr ggtaaaaggt tyraaycgrk gcbnadatwa attcahgatc    300

rnawvaanrk rwttactttk tmrrksmrbg ctahtygtym agtcmgrgra tgacagbths    360

hwhccaatyg cawmatctkg ttytrkggdg aygtygykct gawrtrtctg ccckcttctc    420

gacagatagt agaggaagct ggtggggtgg taactcgcat ggayggtgga gagtttacgg    480

tcttcgatcg ctctgttcyt gkttccaacg gacttgktca tggacaggtt tgtttgttgt    540

saacaatttg gcatattgtt tgtggykttc atggacaggt tttgttctta gtgttgtctg    600

tgtggacagc ttttggaycg gatcggccct cctactgaag accttaagaa gaaagggatc    660

gacttctcgt tgtggttcaa gcctgacaat accckacyga cttttgagcg caycaaggca    720

ccaccaccag ccatkgccac cataataaag cagccatcat ttkkdrrrvm               770


<210> SEQ ID NO 129
<211> LENGTH: 242
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA00521.3

<400> SEQUENCE: 129

arttcccatg aaaaaggaga ccrgkatgct tttgtatcaa tgcttgaggc actatgcaat     60

gcagaaaaga caacagaggc tattgatcta ctgcatatga tgcctgaaaa ggggattact    120

acagatgttg gaatgtataa tatgatmttt tctgctcttg ggaagctgaa gcaggtgtct    180

ttcatgagca gcctctatga tacgatgaga gccaatggtg ttgttcctga tgttttcacg    240

ta                                                                   242


<210> SEQ ID NO 130
<211> LENGTH: 637
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PHM5599.20
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(31)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (46)..(47)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (50)..(51)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (58)..(58)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (60)..(60)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (63)..(65)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (69)..(69)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (81)..(81)
<223> OTHER INFORMATION: n is a, c, g, or t
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (196)..(196)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (629)..(629)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 130

aaaaaaagyg sagdvvkrrk rmbdwgbymn nkmrramrvr raavvnnddn nrrrrddndn 60

ddnnndrvnr hdvrrrarad nccvartymd rrmkarvrrv ggatccvgtg ccgssgvmra 120

ccggttyrav gcyatcsgva ccstbgtccc gsgsatggtc aagctggtgg mggamacmrc 180

cgamcavgty cwhsrnttyg argkkccgga gatgatagag agtaagctag ctagsamrcr 240

mtbrwytyag gamtgswtgt watctwaatc ttaaaaaaat satttgcttt gcyaggggac 300

cggttckcgt ggttcaarga cgargagttc gcgaggcaga cgatcgcggg gctmaacccg 360

ctgtgcatcc agctgctgac ygagttcccc atcaagagca agctggaccc ggaggtgtac 420

gggccagcrg agtccgccat caccaaggag atcctggaga agcagatgaa cggcscgytg 480

accstggagc aggcgctggc ggcgaagcgg ctgttcatcc tggactacca cgacgtgttc 540

ctgccctacg tgcacaaggt gcggagctgc aggackcgac gctctacgcc tsssgcaccr 600

tctcttcstg acgrmcbkya ckdbshhdnb sgkkdwa 637

<210> SEQ ID NO 131
<211> LENGTH: 307
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA00193.2

<400> SEQUENCE: 131

actttmcrgg ccacaccaat tctgcttggt tcttgaagat acattcttcc tatggtgccm 60

cctatataaa agccatttct ggttatgttt atccttgaca tgtcaacaga tyagtgttgg 120

gttgcagtca tgcggtcctt aagtcymgga gaaggcgaga agtcattgct kctagcattg 180

tgatcgtcgg ccacaagtaa tcwaaaagtg agagctactt gttcctagca aatggagaag 240

ggcgatatat aggttkatga tcaaattcag tgtatgcaag cagcatattt tgtttagagw 300

tagcttt 307

<210> SEQ ID NO 132
<211> LENGTH: 189
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA00445.22

<400> SEQUENCE: 132

acaacctact agcgtcatgt tcttttttty ttcttctttc ccttacaatc ccttagttct 60

tgcaagcaga ggtgtacata taastaawtt ctggtgattg actgatcttc tttkttctgg 120

caaacaaytg caggccgcac aagcttcagg ccgtgtgcaa aagtggggcg gcaaaggcac 180

cgatgaagt 189

<210> SEQ ID NO 133
<211> LENGTH: 202
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:

<223> OTHER INFORMATION: PZA02151.3

<400> SEQUENCE: 133

gtccacagrg gaaggagagg tgggtacaac aagagtcctg tacggagccg ttcacccccc 60

gccaggaaaa ggtcacmtag cgatcgtgca cggtcagttt cyaggagcca cctttctagg 120

tcagtatcaa agtctccacc agtgcatcat ccctcsccac ttgattctcc atctctggag 180

cgtgcaagtg atggaaatct cg 202

<210> SEQ ID NO 134
<211> LENGTH: 671
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PHM15427.11
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(8)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (58)..(58)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (656)..(657)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (659)..(659)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 134

anannnnnan tanggaraar aatmwkggrr agytttkrad rabsgwwrgt twrggggnah 60

amaayyaamg gtwggatcaa agamrahwgg gktaccmggr acggggrgkt tyttggsatt 120

tttgtytgsa ahhamttytg maagcytgcc caggggttam tttytcctgk tatsgvaccg 180

aaagcscgkc amgacgacgg cagcctggac ctgattctcg tccatggaag cggcaggytg 240

agactgtttt gsttcyttgt tgcctatcag ytctgctggc atcttctrct cccctacgtg 300

gaatatgtca aggtatgtat cgtgactttc tttgtatctg tttacagcgc ttgttgcggc 360

ggttcatgta cctatagggc ttagtagata tccttgagct tagtagcatg ctctttccta 420

gaacayagga ctccatcagt ttgtcwtggc ttcttagatg mccgtgcact gatgtggyat 480

tttgttgttg cgrcaatgat tgctcgcaga taaaagaagt gaaggttagg ccagttggca 540

gtacccacag tggttgtggy gtcgacggtg agcttctkga tggagagsgc ggtgctgaat 600

ggcagtgctc gctgcttcca gmacaaggca ggctgcttgc mrgatccbgk syrvbnnrnk 660

kkgaaaraaa a 671

<210> SEQ ID NO 135
<211> LENGTH: 242
<212> TYPE: DNA
<213> ORGANISM: artificial

<220> FEATURE:
<223> OTHER INFORMATION: PZA00521.3

<400> SEQUENCE: 135

arttcccatg aaaaaggaga ccrgkatgct tttgtatcaa tgcttgaggc actatgcaat 60

gcagaaaaga caacagaggc tattgatcta ctgcatatga tgcctgaaaa ggggattact 120

acagatgttg gaatgtataa tatgatmttt tctgctcttg ggaagctgaa gcaggtgtct 180

ttcatgagca gcctctatga tacgatgaga gccaatggtg ttgttcctga tgttttcacg 240

ta 242

<210> SEQ ID NO 136
<211> LENGTH: 244
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA02207.1

<400> SEQUENCE: 136

tbssssytca ctaagtgtga ttgtaacagt ggtacctctt gtgttctgtg ttccgcgatg 60

ttgcagttgg ttgcttgatc gaaagatgtt tcarcctccc atctgctagc tatgatacag 120

atggtycctg ataataatga tgacatattc tgtgatggat gccacrrcat tttttkkttt 180

tgtttttgca ttcagatatt tcrgcttcct krtagtttta catgtcccaa ctaggaatga 240

gaag 244

<210> SEQ ID NO 137
<211> LENGTH: 581
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PHM565.31
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(6)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (514)..(514)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (519)..(521)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (532)..(532)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (535)..(536)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (538)..(539)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (541)..(543)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (545)..(545)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:

<221> NAME/KEY: misc_feature
<222> LOCATION: (547)..(548)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (550)..(550)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (552)..(556)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (558)..(558)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (562)..(562)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (569)..(569)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (572)..(572)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (575)..(576)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (580)..(580)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 137

ttkvnnbnwh mavrctgaag attgctgaag gagtgggagt ctagcaaayy wttccgtgtc 60

ccaaacgtcc tgctcacagg gtaccgccag aaggccttgc tggacarggc cgagatgctg 120

ctcgacggct tcttgaagaa gggaaagacg cctccttcga ccagctgggg gatygtggca 180

atcggctatg cggagaaagg tgatgtggcg aaagcttatg agatgaccaa gaacgccctc 240

tctgtgcacg cccccaatac tggctggatc cctaggcctt ccatgcttga gatgatactt 300

aagtacytcg gagacgaggg ggaggtcaak gatgkhkaag cttkcgttag tcwgctgaaa 360

gctgctgtgc castggactc tgatatgacc gaggctttgt ckagggctck tkcsagggaa 420

daaakgawkg ctraaraggc arcggaakct cctcgcgggg atbwtattgc ctrarctbgy 480

wktcsgtktt tcascgctkc kycyvaawkg tcwnytbwnn nhyhcradhb dnbbnnhnnb 540

nnnynhnnhn vnnnnnynbh hnkbryyync tnttnncgcn a 581

<210> SEQ ID NO 138
<211> LENGTH: 215
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA03578.1
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (56)..(56)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 138

atgcagcaga gaatactgtg gaagktgayg ataagaaaga ggaagccccw gctgtngatg 60

cagcagagaa gaaygaggaa ggtgatgata agaaagagga ggagccccct gcagagaara 120

ctgttgagaa agaggtggtc cctgctgtag atgcagcaga gaatactgaa caaagcaccg 180

gtgggcaagc acagcctaay gatgttgstg cccca 215

<210> SEQ ID NO 139
<211> LENGTH: 999
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PZA00300.14
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (225)..(529)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 139

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ggtyrtggtc katctctcat gkgttacrst tttacgctay gtatgggtga cagtskaasm 180

stctaasggt tttrttgwga agwtttttc ttaatacaat acwynnnnnn nnnnnnnnnn 240

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 300

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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 420

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 480

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnna ggrgttrtct 540

tagccywcag gtcattttkt tacmgtctga atttcttaya ctttytaggt cagtagtaac 600

ttgtagattt ygacttgatt ttcacaggcc tgattaatgc attgaarytt atccarcmka 660

tcaargacaa atacmcaggt aycacttatg cagatttgtt ccagttagca agtgctacgg 720

cgattgaggt cactgtcctt tctctgatta agtatctgac ttggtcactt katcactcaa 780

gtctatgyag tcatatgttt tgtcaatcac atgatacagg aagctggtgg tccaaaamtt 840

ccaatgaaat atggacgkgt tgatgtcaca gcakctgarc agtgtccrcc cgaggggagg 900

cttccyggtc agtgtttcya atgggttctt cattccatat caatgtttca ttrttgtttt 960

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caaatgcctc cccggagctc atcaacaggc tgatcccaga ccatgctagg cggcatcttg 180

ggctcacttt attgcccacc rctggaccat aggcgaaggc tctatggtgt ttaaaccttg 240

ctctttctga ttcttcgttg tgccataggc aattcaaggt gtagaatctg accattattg 300

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<223> OTHER INFORMATION: PZA01563.1

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ggtttgtgtg cacatggtgg tgggcagggk ctagagggtt tathtttrgg ttattttcsy    180

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<210> SEQ ID NO 143
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gtagcctcta taag                                                      134
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What is claimed:

1. A method for determining an ear productivity trait in maize, said method comprising:

isolating genomic DNA from a maize plant, germplasm, pollen, or seed;

analyzing genomic DNA from the maize plant, germplasm, pollen, or seed for the presence of a molecular marker linked to a quantitative trait locus (QTL) associated with an ear productivity trait in maize, wherein the molecular marker is selected from the group consisting of L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.locl 14, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_35511, SNP_98111, SNP_23951, SNP_79262, SNP_19249, SNP_9084, SNP_99055, SNP_77055, SNP_45551, SNP_30953, SNP_84678, SNP_89298_2, SNP_32823, SNP_4623, SNP_90941, SNP_81248, SNP_82913, SNP_93907, SNP_90380, SNP_49724, SNP_51496, SNP_11948, SNP_18689, SNP_61221, SNP_105143, SNP_84372, SNP_27764, SNP_95039, SNP_75795, SNP_70805, SNP_43846, SNP_98032, SNP_63437, SNP_94161, SNP_34738, SNP_88270, SNP_2880, SNP_36300, and SNP_77712;

detecting at least one molecular marker that is associated with an ear productivity trait; and

selecting a maize plant having the ear productivity trait.

2. The method according to claim **1**, wherein the ear productivity trait is kernel row number (KRN) and the marker is selected from the group consisting of L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.locl 14, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP_77055, SNP_81248, SNP_82913, SNP_90380, SNP_11948, SNP_61221, SNP_70805, SNP_94161, SNP_2880, and SNP_36300.

3. The method according to claim **1**, wherein the ear productivity trait is cob weight (CW) and the marker is selected from the group consisting of SNP_98111, SNP_32823, SNP_4623, SNP_90941, SNP_27764, SNP_95039, SNP_75795, SNP_34738, and SNP_77712.

4. The method according to claim **1**, wherein the ear productivity trait is cob diameter (CD) and the marker is selected from the group consisting of SNP_90941, SNP_82913, SNP_93907, SNP_105143, SNP_43846, SNP_98032, SNP_88270, and SNP_77712.

5. The method according to claim **1**, wherein the ear productivity trait is cob length (CL) and the marker is selected from the group consisting of SNP_35511, SNP_19249, and SNP_49724.

6. The method according to claim **1**, wherein the ear productivity trait is kernel weight (KW) and the marker is selected from the group consisting of SNP__79262, SNP__9084, SNP__93907, and SNP__84372.

7. The method according to claim **1**, wherein the ear productivity trait is kernel count (KC) and the marker is selected from the group consisting of SNP__9084, SNP__99055, SNP__45551, SNP__89298__2, SNP__51496, and SNP__63437.

8. The method of claim **1**, wherein said selecting occurs as part of a breeding program to improve a maize variety's ear productivity.

9. The method of claim **8**, wherein the breeding program comprises crossing, making hybrids, backcrossing, self-crossing, double haploid breeding, and/or combinations thereof.

10. A method for producing a maize line having a desired ear productivity trait, said method comprising:

providing a first maize line having a molecular marker selected from the group consisting of L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP__35511, SNP__98111, SNP__23951, SNP__79262, SNP__19249, SNP__9084, SNP__99055, SNP__77055, SNP__45551, SNP__30953, SNP__84678, SNP__89298__2, SNP__32823, SNP__4623, SNP__90941, SNP__81248, SNP__82913, SNP__93907, SNP__90380, SNP__49724, SNP__51496, SNP__11948, SNP__18689, SNP__61221, SNP__105143, SNP__84372, SNP__27764, SNP__95039, SNP__75795, SNP__70805, SNP__43846, SNP__98032, SNP__63437, SNP__94161, SNP__34738, SNP__88270, SNP__2880, SNP__36300, and SNP__77712, the molecular marker mapping to a genomic locus associated with a desired ear productivity trait;

introgressing the desired ear productivity trait into a maize line; and

selecting a maize line having the desired ear productivity trait.

11. The method according to claim **10**, wherein the ear productivity trait is kernel row number (KRN) and the marker is selected from the group consisting of L00401, L004011, c 1.loc28, L01176, c 2.loc70, c 2.loc66, L01157, L00033, L000331, L00198c, L00198c1, c 3.loc52, L01138, L011381, c 4.loc126, c 4.loc1261, L00280, L00133, c 4.loc106, L01028, L010281, L00576, L005761, c 4.loc52, c 4.loc521, c 4.loc114, L00589, L00134, c 5.loc47, c 5.loc471, L00221, L002211, c 5.loc73, L00110, c10.loc51, c10.loc50, SNP__77055, SNP__81248, SNP__82913, SNP__90380, SNP__11948, SNP__61221, SNP__70805, SNP__94161, SNP__2880, and SNP__36300.

12. The method according to claim **10**, wherein the ear productivity trait is cob weight (CW) and the marker is selected from the group consisting of SNP__98111, SNP__32823, SNP__4623, SNP__90941, SNP__27764, SNP__95039, SNP__75795, SNP__34738, and SNP__77712.

13. The method according to claim **10**, wherein the ear productivity trait is cob diameter (CD) and the marker is selected from the group consisting of SNP__90941, SNP__82913, SNP__93907, SNP__105143, SNP__43846, SNP__98032, SNP__88270, and SNP__77712.

14. The method according to claim **10**, wherein the ear productivity trait is cob length (CL) and the marker is selected from the group consisting of SNP__35511, SNP__19249, and SNP__49724.

15. The method according to claim **10**, wherein the ear productivity trait is kernel weight (KW) and the marker is selected from the group consisting of SNP__79262, SNP__9084, SNP__93907, and SNP__84372.

16. The method according to claim **10**, wherein the ear productivity trait is kernel count (KC) and the marker is selected from the group consisting of SNP__9084, SNP__99055, SNP__45551, SNP__89298__2, SNP__51496, and SNP__63437.

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